

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 01:30:31 ; Search time 85 Seconds
(without alignments)
805.774 Million cell updates/sec

Title: US-09-846-637C-4
Perfect score: 2619
Sequence: 1 MADYLISGGSYVPDDGLTA.....SSAQVEGVSLHSYEKRLF 514

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002: *
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2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
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22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2605	99.5	514	11	AA05432	
2	2605	99.5	514	23	AAE18189	Human IMPDH, Hom
3	2595	99.1	514	23	AAE18186	Human wild-type, t
4	2595	99.1	514	23	AAU10695	Human wild-type, t
5	2559	97.7	514	11	AA05431	Reference sequence
6	2234	85.3	514	23	AAE18188	Chinese hamster IM
7	2229	85.1	514	23	AAE18257	Human wild-type in
8	2227	85.0	514	23	AAE18258	Human type I inosi
9	2222	84.8	514	23	AAE18185	Human type I IMPDH
10	2202	84.1	514	23	AAE18190	Human wild-type, t

11	2201	84.0	514	23	AAE18191	Human wild-type, t
12	2141.5	81.8	604	22	ABG22269	Novel human diapo
13	2115.5	80.8	509	23	AAU99361	Human oxidoreducta
14	1862	71.1	384	23	AAE18165	Human type II inos
15	1861.5	71.1	385	23	AAE18179	Human modified ino
16	1860.5	71.0	385	23	AAE18177	Human modified ino
17	1860	71.0	384	23	AAE18174	Human type II inos
18	1859.5	71.0	385	23	AAE18181	Human type II IMPD
19	1858	70.5	384	23	AAE18169	Human modified ino
20	1857.5	70.5	385	23	AAE18182	Human modified ino
21	1857.5	70.5	385	23	AAE18183	Human type II IMPD
22	1857	70.5	384	23	AAE18167	Human modified ino
23	1856	70.5	384	23	AAE18166	Human modified ino
24	1856	70.5	384	23	AAE18170	Human modified ino
25	1856	70.5	384	23	AAE18172	Human type II inos
26	1855.5	70.6	385	23	AAE18176	Human modified ino
27	1855.5	70.6	385	23	AAE18178	Human modified ino
28	1855.5	70.6	385	23	AAE18180	Human modified ino
29	1855	70.6	384	23	AAE18168	Human modified ino
30	1853	70.6	384	23	AAE18173	Human modified ino
31	1852	70.7	384	23	AAE18171	Human modified ino
32	1851.5	70.7	385	23	AAE18184	Human modified ino
33	1764.5	67.4	537	22	ABBS58547	Drosophila melanog
34	1764.5	67.4	537	22	ABBS5768	Drosophila melanog
35	1644	62.8	384	23	ABE18175	Human type I inosi
36	1524	58.2	430	22	ABG23731	Novel human diapo
37	1210.5	46.2	371	20	AAV08965	A. gossypii inosin
38	1155	44.1	502	21	AAG30888	Arabidopsis thalia
39	1114.5	42.6	503	21	AAG20989	Arabidopsis thalia
40	1106.5	42.2	503	21	AAG43108	Arabidopsis thalia
41	1066	40.7	287	22	ABG07490	Novel human diapo
42	1043.5	39.8	403	22	AAG70679	S cerevisiae apopt
43	1021	39.0	443	21	AAG30889	Arabidopsis thalia
44	996	38.0	435	21	AAG30890	Arabidopsis thalia
45	987.5	37.7	444	21	AAG20990	Arabidopsis thalia

ALIGNMENTS

RESULT 1					
AA05432					
ID	AA05432	standard; protein; 514 AA.			
XX					
AC	AA05432;				
XX					
DT	31-AUG-1990	(first entry)			
XX					
DE	Human IMPDH.				
XX					
KW	Inosine 5'-mono-phosphate dehydrogenase; hepatomas;				
KW	guanosine monophosphate.				
XX					
OS	Homo sapiens.				
XX					
PN	W09001545-A.				
XX					
PD	22-FEB-1990.				
XX					
PF	02-AUG-1989;	89WO-0000344.			
XX					
PR	12-AUG-1988;	88US-0232302.			
XX					
PA	(ARCH-) ARCH. DEV. CORP.				
XX					
PI	Collart ER, Huberman E;				
XX					
DR	WPI; 1990-083504/11.				
DR	P-PSDB; AA05432.				
XX					
PT	DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -				
PT	used to detect high levels of enzyme activity of tumour cells,				
PT	esp. hepatomas, and to produce guanosine monophosphate.				

xx Claim 8; Fig 1; 51pp; English.
ps
xx
cc A 35 aa segment corresponds to deduced aa residues 336-370 in
cc both the human and Chinese hamster proteins.
cc See also AAQ03541.
xx
sq Sequence 514 AA;

Query Match 99.5%; Score 2605; DB 11; Length 514;
Best Local Similarity 99.6%; Pred. No. 2.8e-246;
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADYLLISGGSYVPDDGLTAAQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSAITKKIT 60
Db 1 MADYLLISGGSYVPDDGLTAAQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLVSSPMDTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKKEOGFITDPVV 120
Db 61 LKTPLVSSPMDTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKKEOGFITDPVV 120
QY 121 LSPKDRVDFEAKARHGFSGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLKEIMT 180
Db 121 LSPKDRVDFEAKARHGFSGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLKEIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
QY 241 KKQLLGAIGTTHEDDKYRLDLAQAGVDVVLDSSQGSNIFQINMIKYIKDKYPNLQVI 300
Db 241 KKQLLGAIGTTHEDDKYRLDLAQAGVDVVLDSSQGSNIFQINMIKYIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITIQEVLACGRPOATAVYKVEYARRFGVP 360
Db 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITIQEVLACGRPOATAVYKVEYARRFGVP 360
QY 361 VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRYFSEADKIKVAQVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTQVR 480
Db 421 DKHLSSQNRYFSEADKIKVAQVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTQVR 480
QY 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSEYKRLF 514
Db 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSEYKRLF 514

RESULT 2
AAE18189
ID AAE18189 standard; Protein; 514 AA.
XX
AC AAE18189;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human wild-type, type II IMPDH #2.
XX
KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW enzyme; therapy.
XX
OS Homo sapiens.
XX
PN WO200185952-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US15457.
XX
PR 10-MAY-2000; 2000US-203448P.

xx
pa (BRIM) BRISTOL-MYERS SQUIBB CO.
xx
pi Krystek SR, Sheriff S, Wilmer MR, Hollenbaugh DL, Yan N;
pi Mouravieff JE, Einspahr HM, Kish K;
xx
dr WPI; 2002-164105/21.
xx

PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies -
xx
ps Claim 55; Page 154-156; 161pp; English.

cc The invention relates to modified inosine 5'-monophosphate dehydrogenase
cc (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
cc substituted for a subdomain of a wild-type IMPDH polypeptide. The
cc modified IMPDH polypeptides are useful for drug discovery, for
cc therapeutic, diagnostic and prognostic procedures for detecting or
cc quantifying modified IMPDH polypeptides and their corresponding nucleic
cc acids. IMPDH polypeptides are also useful for generating antibodies, as
cc diagnostic and prognostic markers of diseases, as targets for various
cc therapeutic modalities, and to identify and isolate ligands and other
cc agents that bind to modified IMPDH. These antibodies may be used in
cc diagnostic assays, imaging methodologies, therapeutic methods in the
cc management of cancer or other proliferative-type diseases, and in
cc purifying modified IMPDH polypeptides and for isolating related
cc molecules such as wild type and mutant IMPDH polypeptides. The present
cc sequence is human wild-type type II IMPDH.
xx

sq Sequence 514 AA;

Query Match 99.5%; Score 2605; DB 23; Length 514;
Best Local Similarity 99.6%; Pred. No. 2.8e-246;
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADYLLISGGSYVPDDGLTAAQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSAITKKIT 60
Db 1 MADYLLISGGSYVPDDGLTAAQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLVSSPMDTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKKEOGFITDPVV 120
Db 61 LKTPLVSSPMDTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKKEOGFITDPVV 120
QY 121 LSPKDRVDFEAKARHGFSGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLKEIMT 180
Db 121 LSPKDRVDFEAKARHGFSGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLKEIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
QY 241 KKQLLGAIGTTHEDDKYRLDLAQAGVDVVLDSSQGSNIFQINMIKYIKDKYPNLQVI 300
Db 241 KKQLLGAIGTTHEDDKYRLDLAQAGVDVVLDSSQGSNIFQINMIKYIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITIQEVLACGRPOATAVYKVEYARRFGVP 360
Db 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITIQEVLACGRPOATAVYKVEYARRFGVP 360
QY 361 VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRYFSEADKIKVAQVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTQVR 480
Db 421 DKHLSSQNRYFSEADKIKVAQVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTQVR 480
QY 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSEYKRLF 514
Db 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSEYKRLF 514

RESULT 3
AAE18186
ID AAE18186 standard; protein; 514 AA.
XX
AC AAE18186;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human wild-type, type II IMPDH #1.
XX
KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW enzyme; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 111..243
FT /label= sub_domain
XX
PD WO200185952-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US15457.
XX
PR 10-MAY-2000; 2000US-203448P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Krystek SR, Sheriff S, Witmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;
XX
DR WPI; 2002-164105/21.
XX
PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies
XX
PS Claim 55; Fig 2; 161pp; English.
XX
CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or
CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other
CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the
CC management of cancer or other proliferative-type diseases, and in
CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is human wild-type type II IMPDH.
XX
SQ Sequence 514 AA;
Query Match 99.1%; Score 2595; DB 23; Length 514;
Best Local Similarity 99.2%; Pred. No. 2.7e-245;
Matches 510; Conservative 0; Mismatches 4; Inels 0; Gaps 0;

QY 121 LSPKDRVRDVFEEKARHGFSGIPITDTGMRGSLVGISSRDIDFLKEEHDCLFEEIMT 180
DB 121 LSPKDRVRDVFEEKARHGFSGIPITDTGMRGSLVGISSRDIDFLKEEHDCLFEEIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
DB 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
QY 241 KKQLLCGAAGCTHEDDKYRLDLAQAGVDVVLDDSSQNSIFQIMIKYIKDKYPNLQVI 300
DB 241 KKQLLCGAAGCTHEDDKYRLDLAQAGVDVVLDDSSQNSIFQIMIKYIKDKYPNLQVI 300
QY 301 GGNVTTAAQAKNLIDAGVDALRVGMSGSGICITQEVLAGCRPQATAVYKVEYARRFGVP 360
DB 301 GGNVTTAAQAKNLIDAGVDALRVGMSGSGICITQEVLAGCRPQATAVYKVEYARRFGVP 360
QY 361 VIADGGIONVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 420
DB 361 VIADGGIONVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 420
QY 421 DKHLSSQNRFFSEADKIKVAQGVSGAVODKGSIHKFPYLIAGIOHSCODIGAKSLTQVR 480
DB 421 DKHLSSQNRFFSEADKIKVAQGVSGAVODKGSIHKFPYLIAGIOHSCODIGAKSLTQVR 480
QY 481 AMMSGELKFEKRTSSAOVEGGVHSLHSEKRLF 514
DB 481 AMMSGELKFEKRTSSAOVEGGVHSLHSEKRLF 514
RESULT 4
AAU10695
ID AAU10695 standard; protein; 514 AA.
XX
AC AAU10695;
XX
DT 25-FEB-2002 (first entry)
XX
DE Reference sequence for human IMPDH2 polypeptide.
XX
KW Human; single nucleotide polymorphism; SNP; IMPDH2; chromosome 3p21.2;
KW IMP dehydrogenase 2; haplotyping; genotyping; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200177363-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US11851.
XX
PR 11-APR-2000; 2000US-196248P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi Jr, Koshy B, Lee HH, Stephens JC;
PI N-PSDB; AAS18240.
XX
DR WPI; 2002-041297/05.
DR N-PSDB; AAS18240.
XX
PT New isolated polynucleotide having polymorphic variant of IMP2
PT dehydrogenase gene, useful for studying expression of the gene in vivo,
PT and for testing efficacy of therapeutic agents for cancer in biological
PT system
XX
PS Disclosure; Fig 3; 70pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human IMP dehydrogenase 2 (IMPDH2) gene located on
CC chromosome 3p21.2, and methods for haplotyping and/or genotyping the
CC IMPDH2 gene in an individual. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the IMPDH2 gene
CC polymorphisms. The polynucleotides and screened compounds are

CC useful for (developing) treatment of diseases associated with IMPDH2
CC activity, such as cancer. The present sequence represents a reference
CC sequence for the IMPDH2 polypeptide.

XX
SQ Sequence 514 AA;

Query Match 99.1%; Score 2595; DB 23; Length 514;
Best Local Similarity 99.2%; Pred. No. 2.7e-245;
Matches 510; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADYLISGTSYVPDDGLTAQQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60
|||
Db 1 MADYLISGTSYVPDDGLTAQQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGIFIHNCTPEFQANEVRKVKKYEQGFTDPVY 120
|||
Db 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGIFIHNCTPEFQANEVRKVKKYEQGFTDPVY 120
QY 121 LSPKDRYRDVFEAKARHGF CGIPITDTGRMGSRVLVGIISSRDIDFLKEEHCFLKEEIMT 180
|||
Db 121 LSPKDRYRDVFEAKARHGF CGIPITDTGRMGSRVLVGIISSRDIDFLKEEHCFLKEEIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
|||
Db 181 KREDLVVAPAGITLKEANEILQRSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
QY 241 KKQLLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIKYYIKDKYPNLQVI 300
|||
Db 241 KKQLLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIKYYIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGSGSICITIQEVLAACGRPOATAVYKVSEYARFGVP 360
|||
Db 301 GGNVVTAAQAKNLIDAGVDALRVGSGSICITIQEVLAACGRPOATAVYKVSEYARFGVP 360
QY 361 VIADGGIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
|||
Db 361 VIADGGIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRIFYSEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480
|||
Db 421 DKHLSSQNRIFYSEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480
QY 481 AMMYSGELEKFEKRTSSAQVEGGVHSLHSEKRLF 514
|||
Db 481 AMMYSGELEKFEKRTSSAQVEGGVHSLHSEKRLF 514

RESULT 5

AAR05431
ID AAR05431 standard; protein; 514 AA.

XX
AC AAR05431;
XX
DT 31-AUG-1990 (first entry)
XXR Chinese hamster IMPDH.

XX Inosine 5'-mono-phosphate dehydrogenase; hepatomas;
KW guanosine monophosphate.
XX
OS Cricetulus sp.

PN W09001545-A.

XX PD 22-FEB-1990.

XX PF 02-AUG-1989; 89WO-0000344.

XX PR 12-AUG-1988; 88US-0232302.

XX PA (ARCH-) ARCH. DEV. CORP.

XX PI Collart FR, Huberman E;

XX
DR WPI; 1990-083504/11.
DR N-PSDB; AAQ03541.

XX
PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
PT used to detect high levels of enzyme activity of tumour cells,
PT esp. hepatomas, and to produce guanosine monophosphate.

XX PS Claim 8; Fig 2; 51pp; English.

XX CC A 35 aa segment corresponds to deduced aa residues 336-370 in
CC both the human and Chinese hamster proteins.
CC See also AAQ03540.

XX
SQ Sequence 514 AA;

Query Match 97.7%; Score 2559; DB 11; Length 514;
Best Local Similarity 98.1%; Pred. No. 9.3e-242;
Matches 504; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MADYLISGTSYVPDDGLTAQQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60
|||
Db 1 MADYLISGTSYVPDDGLTAQQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGIFIHNCTPEFQANEVRKVKKYEQGFTDPVY 120
|||
Db 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGIFIHNCTPEFQANEVRKVKKYEQGFTDPVY 120
QY 121 LSPKDRYRDVFEAKARHGF CGIPITDTGRMGSRVLVGIISSRDIDFLKEEHCFLKEEIMT 180
|||
Db 121 LSPKDRYRDVFEAKARHGF CGIPITDTGRMGSRVLVGIISSRDIDFLKEEHCFLKEEIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
|||
Db 181 KREDLVVAPAGITLKEANEILQRSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
QY 241 KKQLLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIKYYIKDKYPNLQVI 300
|||
Db 241 KKQLLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIKYYIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGSGSICITIQEVLAACGRPOATAVYKVSEYARFGVP 360
|||
Db 301 GGNVVTAAQAKNLIDAGVDALRVGSGSICITIQEVLAACGRPOATAVYKVSEYARFGVP 360
QY 361 VIADGGIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
|||
Db 361 VIADGGIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRIFYSEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480
|||
Db 421 DKHLSSQNRIFYSEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480
QY 481 AMMYSGELEKFEKRTSSAQVEGGVHSLHSEKRLF 514
|||
Db 481 AMMYSGELEKFEKRTSSAQVEGGVHSLHSEKRLF 514

RESULT 6
AAE18188
ID AAE18188 standard; protein; 514 AA.

XX
AC AAE18188;

XX
DT 07-MAY-2002 (first entry)

XX DE Human wild-type inosine 5'-monophosphate dehydrogenase (IMPDH).

XX KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW enzyme; therapy.

XX
OS Homo sapiens.

Best Local Similarity 83.3%; Pred. No. 2.2e-209;
Matches 428; Conservative 39; Mismatches 47; Indels 0; Gaps 0;

QY	1	MADYLISGSGTSYVPDDGLTAOQLFENCGBDGLTYNDLFLPGIYIDFTADQVDLTSALTRKIT	60
Dd	1	MADYLISSGTGYVPEDGLTAOQLFASADGLTYNDLFLPGIFIDEFADEVDLTSALTRKIT	60
QY	61	LKTPLYVSSPMDVTVEAGMAIAMALTGGIGIFIHNNCTPEFOANEVRKKVKEOGFITDPVY	120
Dd	61	LKTPLISSPMDVTTEADMAIAMALMGIGIFIHNNCTPEFOANEVRKKVKNFEOGFITDPVY	120
QY	121	LSPKDRVDFEAKARHGFCSPIPTDTGRMGSRLVGITISSRIDFLKEEHDCFLEETMT	180
Dd	121	LSPSHTVGDVLAEAKMRHGFSGPITETGTMSGSKLVGIVTSRDIIDLAEKDHTTLSEYMT	180
QY	181	KREDLVVAPRSITLKEANEILORSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA	240
Dd	181	PRIELVVAPEGVTLKEANEILORSKKGKLPVINDCDELVAIIARTDLKKNRDYPLASKDS	240
QY	241	KKOLLGAAGITHEDDKYRLDLLAOAGVDVVLLDSSQSNGSTFQINMIKYIKDKYPNLOVI	300
Dd	241	OKOLLGAAGVTRREDDKYRLDLLTAGVDVIVLDSSQSNGSNYYQIAMVHYIKOKYPHLQVI	300
QY	301	GGNVNTAAQAKNLIDAGVDALRVGMGSGSICIIQEVLACGRPOATAVYKVYEYARRRGVP	360
Dd	301	GGNVNTAAQAKNLIDAGVDGLRVGMCGSICITQEVMACGRROGTAVYKVAEYARRRGVP	360
QY	361	VIADEGIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKRYRGMGSLDAM	420
Dd	361	IADGIGIQYGVHVVKALALGASTVMGSLLAATTEAPGEYFFSDGVRLLKRYRGMGSLDAM	420
QY	421	DKHLSSQNRYFSEADKIKVAQGVSAGVODKGSIHKFVPYLIAGIOHSQCODIGAKSLTOVR	480
Dd	421	EKSSSSQKRIFYSEGDKVKIAQGVSGSIQDKGSIQKFPVPLYIAGIOHCQDIGARSLSVLR	480
QY	481	AMMYSGELKEFKRTSSAQVEGCVSHLSHEYKRLF 514	
Dd	481	SMYSGELKEFKRTMSAQIEGCVGHLSHEYKRLY 514	

RESULT 8	
AAE18258	
ID	AAE18258 standard; Protein; 514 AA.
XX	
AC	AAE18258;
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	Human type I IMPDH mutant, N109K.
XX	
KW	Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW	proliferative-type disease; cancer; imaging methodology; cytostatic;
KM	enzyme; therapy; mutant; muteln.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 109
FT	/note= "Wild-type Asn is substituted with Lys"
XX	
PN	WO200185952-A2.
XX	
PD	15-NOV-2001.
XX	
PF	10-MAY-2001; 2001WO-US15457.
XX	
PR	10-MAY-2000; 2000US-203448P.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Krystek SR, Sheriff S, Witmer MR, Hollenbaugh DL, Yan N;
PI	Mouravieff JE, Einspahr HM, Kish K;

XX WPI; 2002-164105/21.
 DR
 XX
 XX New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
 PT having an oligo-peptide domain substituted for a subdomain of a
 PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
 PT antibodies -
 XX
 PS Disclosure; Page -; 161pp; English.

The invention relates to modified inosine 5'-monophosphate dehydrogenases (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain substituted for a subdomain of a wild-type IMPDH polypeptide. The modified IMPDH polypeptides are useful for drug discovery, for therapeutic, diagnostic and prognostic procedures for detecting or quantifying modified IMPDH polypeptides and their corresponding nucleic acids. IMPDH polypeptides are also useful for generating antibodies, as diagnostic and prognostic markers of diseases, as targets for various therapeutic modalities, and to identify and isolate ligands and other agents that bind to modified IMPDH. These antibodies may be used in diagnostic assays, imaging methodologies, therapeutic methods in the management of cancer or other proliferative-type diseases, and in purifying modified IMPDH polypeptides and for isolating related molecules such as wild type and mutant IMPDH polypeptides. The present sequence is human type I IMPDH mutant.

Note: This sequence is not shown in the specification, however this sequence is constructed based on the human wild-type type I IMPDH SEQ.ID.NO.48 (AAE18185) shown in fig 1 of the specification.

SQ Sequence 514 AA;

Query Match	85.0%;	Score 2227;	DB 23;	length 514;
Best Local Similarity	83.3%;	Pred. No. 3.4e-209;		
Matches 428;	Conservative 39;	Mismatches 47;	Indels 0;	Gaps 0;

QY	1	MADYLLISGGISYVPPDDGLTAQÖLFNCGDGLTYNDFLILPGIIDEFTADÖVDLTSLATKKIT	60
Db	1	MADYLLISGGIGYVPEDGGLTAQÖLFASADDLTYNDFLILPGIFIDFIADEVDLTSLATRKIT	60
QY	61	LKTPLVSSPMDVTVEAGMAIAMALTGIGIFIHNNCTPEFQANEVRKKYKEÖGFTDPVY	120
Db	61	LKTPLISSPMDVTVEADMAIAMALMGIGIFIHNNCTPEFQANEVRKKYKEÖGFTDPVY	120
QY	121	LSPKDRVDRVFEAKARHGFCCGIPITDTGRMGSRVLVGIISSRDIDFLKEEHDCFLIEIMT	180
Db	121	LSPSHTVGDVLEAKMRHGFSGIPITETGTMGSKLVGIVTSRDIDFLAEKDHITLSEVMT	180
QY	181	KREDLVAPRSITLKEANEILÖRSKKGLPIVNEDEDELVAIARTDLKKNRDYPLASKDA	240
Db	181	PRIELVAPAGVTLKEANEILÖRSKKGLPIVNDCEDELVAIARTDLKKNRDYPLASKDS	240
QY	241	KKÖLLCGAAGITHEDDKYRLDLLAQGVDPVVLDDSSÖGNSITFQINMIKYIKDKKYPNLÖVI	300
Db	241	ÖKÖLLCGAAGVTHREDDKYRLDLLAQGVDPVVLDDSSÖGNSYÖIAMVHYIKÖKYPHLÖVI	300
QY	301	GGNVVTAQAÖKANLIDAGVDALRVGMSGSGICITQEVLAACGRPQATAVYKVVEYARREGVP	360
Db	301	GGNVVTAQAÖKANLIDAGVDGLRVGMSGSGICITQEVMAACGRPQGTAVYKVAEYARREGVP	360
QY	361	VIADGCIÖNVGHILAKALALGASTVMGSLLAATTEAPGEYEFESDGI RLKKYRGMSLDAM	420
Db	361	IADGCIÖTVGHVYKALALGASTVMGSLLAATTEAPGEYEFESDGVRLKKYRGMSLDAM	420
QY	421	DKHLSSÖNRRYFESEADKIKVAÖGVSAGAVÖDKSGIHKFVPYLIAGIQHSCÖDIGAKSLTÖVR	480
Db	421	EKSSSSÖKRRYFESEGDVKKIAÖGVSIGIQDKSGIÖKFVPYLIAGIQHGÖDIGARSLSVLR	480
QY	481	AMYSGELKEFEKRTSSAQÖVEGGVHSLHSYEKRLE 514	
Db	481	SMYSGELKEFEKRTMSAQÖIEGGVHGLHSYEkRLY 514	

RESULT 9

[illegible]

Db	181	PRIELVAPAGVTLKEANEILQ	RSKKGLPIVND	CDELVAITARTDLKKNRDYPLASKDS	240
QY	241	KQLLCGAAITGHEDDKYRLDLLA	QAGVDVLDSSQ	QNSIFQINMIKYLKDKYPNLQVI	300
Db	241	QKQLLCGAAVGTREDDKYRLDLL	TQAGVDYIVL	SSQNSNYQIAMVHYIKQKYPHLQVI	300
QY	301	GGNVVTAQAQAKNLIDAGVDAL	RVMGSGSICITQ	EVLACGRQOATAVYKVEYARREGVP	360
Db	301	GGNVVTAQAQAKNLIDAGVDGL	RVMGCGSICITQ	EVMACGRPOGTAVYKVAEYARREGVP	360
QY	361	VIADGGIQNVGHIAKALALGAST	VMGSLAATTEAPGEYFFSDGIRL	KYRGMSLDAM	420
Db	361	IIADGGIQTVGSHVVKALALGAST	VMGSLAATTEAPGEYFFSDGIRL	KYRGMSLDAM	420
QY	421	DKHLSSQNRNFESEADKIKVAQ	GSAGAVQDKGSIHKFV	PLYLAGIQHSCQDIGAKSLTQVR	480
Db	421	EKSSSSQKRYRSEGDVKVIAQ	GSVSGSIQDKGSIQKFV	PLYLAGIQHGQDIGARSLSVLR	480
QY	481	AMMYSGELKFEKRTSSAQVEGV	SHSLHSEKRLF	514	
Db	481	SMYSGELKFEKRTMSAQIEG	VHGLHSEKRLY	514	

RESULT 10

AAE1819C

ID AAE18190 standard; Protein; 514 AA.

AC AAE18190;

DT 07-MAY-2002 (first entry)

DE Human wild-type, type I IMPDH #2.

KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW enzyme; therapy.

05 Homo sapiens.

PN W0200185952-A2.

PD 15-NOV-2001.

PF 10-MAY-2001; 2001WO-US15457.

PR 10-MAY-2000; 2000US-203448P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Krystek SR, Sheriff S, Witmer MR, Hollenbaugh DL, Yan N;

PI Mouravieff JE, Einspahr HM, Kish K;

DR WPT; 2002-164105/21.

PT	New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT	having an oligo-peptide domain substituted for a subdomain of a
PT	wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT	antibodies -

PS Claim 55; Page 157-159; 161pp; English.

CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or
CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other
CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the
CC management of cancer or other proliferative-type diseases, and in

CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is human wild-type type I IMPDH.

SQ Sequence 514 AA;

Query Match	84.1%;	Score 2202;	DB 23;	Length 514;
Best Local Similarity	82.1%;	Pred. No. 9.8e-207;		
Matches 422;	Conservative 41;	Mismatches 51;	Indels 0;	Gaps 0;

QY	1	MADYLISGGSYVPPDDGLTAQOLFNCBGDLTYNDFLILPGYIDFTADQVDTLSALTKKIT	60
Db	1	MADYLISGGTGYVPEDGLTAHELFPASADGLTYNDFLILPGFIDFIADEVDTLSALTRKIT	60
QY	61	LKTPLVSSPMDTVTEAGMAIAMALTTGGIGFIHHNCTPEFOANEVRKVKYEOGFTDPVY	120
Db	61	LKTPLISSPMDTVTEADMAIAMALMGIGFIHHNCTPEFOANEVRKVKYEOGFTDPVY	120
QY	121	LSPKDRVDFEAKARHFGCGIPITDTGRMGSRVLGISSRDIDFLKEEHDCFLEEIMT	180
Db	121	LSPSHTVGDVLEAKMRHFGSGIPITETGTMGSKLVGIVTSRDIIDFLAEKDHITLLSEVMT	180
QY	181	KREDLVVAPRSITLKEANEILORSKKGKLPIVENDEDELVAIIARTDLKKNRDYPLASKDA	240
Db	181	PRIELVVAPAGVTLKEANEILQRTKKGKLPIVNDCDELVAIIARTDLKKNRDYPLASKDS	240
QY	241	KKOLLGGAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIKYIKDKYPNLQVI	300
Db	241	OKOLLGGAAGVTRBDKRYRLDLLTQAGVDVIVFHSSQGSNSVQIAMVHYIKOKYPHLQVI	300
QY	301	GGNVYTAQAQAKNLIDAGVDALRVGMSSSICIIOEVLACGRPOATAVYKYVEYARFGVP	360
Db	301	GGNVYTAQAQAKNLIDAGVDGLRVGMGGSICITQEVMACGRPOGTAVYKYAEYARFGVP	360
QY	361	VIADGGIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
Db	361	VIADGGIQTGVGHVVKALALGASTVMGSLLAATTEAPGEYFFSDGVRLLKKYRGMGSLDPM	420
QY	421	DKHLSSQNRIFYSEADKIKVAQGVSGAVODKGSIHKFVPLYIAGIQHSCODIGAKSLTOVR	480
Db	421	EKSSSSQKRYFSEGDVKVIAQGVSGSIQDKGSIQKFVPLYIAGIQHGCODIGARSLSVLR	480
QY	481	AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF	514
Db	481	SMYSGELKFEKRTMSPOIEGGVHGLHSYEKRLY	514

RESULT 11	
AAE18191	
ID	AAE18191 standard; Protein; 514 AA.
XX	
AC	AAE18191;
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	Human wild-type, type I IMPDH #3.
XX	
KW	Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW	proliferative-type disease; cancer; imaging methodology; cytostatic;
KW	enzyme; therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200185952-A2.
XX	
PD	15-NOV-2001.
XX	
PF	10-MAY-2001; 2001WO-US15457.
XX	
PR	10-MAY-2000; 2000US-203448P.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	

PI Krystek SR, Sheriff S, Wiltmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;
XX
DR WPI; 2002-164105/21.

PT	New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT	having an oligo-peptide domain substituted for a subdomain of a
PT	wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT	antibodies
XX	-
PS	Claim 55; Page 159-161; 161pp; English.

Claim 55; Page 159-161; 161pp; English.

The invention relates to modified inosine 5'-monophosphate dehydrogenase (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain substituted for a subdomain of a wild-type IMPDH polypeptide. The modified IMPDH polypeptides are useful for drug discovery, for therapeutic, diagnostic and prognostic procedures for detecting or quantifying modified IMPDH polypeptides and their corresponding nucleic acids. IMPDH polypeptides are also useful for generating antibodies, as diagnostic and prognostic markers of diseases, as targets for various therapeutic modalities, and to identify and isolate ligands and other agents that bind to modified IMPDH. These antibodies may be used in diagnostic assays, imaging methodologies, therapeutic methods in the management of cancer or other proliferative-type diseases, and in purifying modified IMPDH polypeptides and for isolating related molecules such as wild type and mutant IMPDH polypeptides. The present sequence is human wild-type type I IMPDH.

SQ Sequence 514 AA;

Query Match	84.0%;	Score 2201;	DB 23;	Length 514;
Best Local Similarity	82.3%;	Pred. No. 1.2e-206;		
Matches 423;	Conservative 39;	Mismatches 52;	Indels 0;	Gaps 0;

QY	1	MADYLISGGTSYVPDDGLTAOQLFNGCGELTYNDELILPGYIDFTADOVDLTSAJTKKIT	60
Dd	1	MADYLISSGCTGYVPEDGLTAOQLFASADDLTYNDFLILPGFIDFIADDEVDTLSALTRKIT	60
QY	61	LKTPLVSSPMDTVTEAGMAIAMALTGTIGFIHNCTPEFOANEVRKVKKYEQGFTDPVY	120
Dd	61	LKTPLISSPMDTVTEADMAIAMALMGICGFIHNNCTPEFOANEVRKVKNFEQGITDPVY	120
QY	121	LSPKDRVRDVEEAKARHGFCGPIPTDGIRMGSRLVGIISSRDIDLKEEHDCFLEEIMT	180
Dd	121	LSPSHTVGDVLEAKMRHGFSGPITETGTWMSKLVGIIVTSRDIIDLAEKDHTLLSEVMT	180
QY	181	KREDLVAPRSITLKEANEILORSKKGKLPIVNEDELVAIARTDLKKNRDYPPLASKDA	240
Dd	181	PRIELVVAPAGVTLIKEANEILORSKRKGLPIVNDCEDELVAIIARTDLKKNRDYPLASKDS	240
QY	241	KKOLLGGAIGTHEDDKYRLDLLAAGAVDVVVLDSOGNSIFQIINMIKYIKDKYPNLQVI	300
Dd	241	QKOLLGGAIVGTREDDKYRLDLLTOAGADVIVEFHSSQGSNVQIAMVHYIKOKYPHLQVI	300
QY	301	GGNVNTAAQAQAKNLIDAGVDALRVGMSSSICIIOEVLAGCRPOATAVYKYEYARRFGVP	360
Dd	301	GCNVVNTAAQAQAKNLIDAGVDGLRVGMSSSICITOEVMACGRPOGTAVYKYAEYARRFGVP	360
QY	361	VIAADGCIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKRYRGMSLDAM	420
Dd	361	IITADGCIQTGVGHVKALLAGASTVMGSLLAATTEAPGEYFFSDGVRLKRYRGMSLDPM	420
QY	421	DKHLSSONRYFSEADKIKVAQVSAGAVODKSGIHKFVPLYLAGIQHSQCODIGAKSLTOVR	480
Dd	421	EKSSSSQKRYFSEGDVKVIAQVSGSIQDDKSGSIQKFVPLYLAGIQHGCDIGARSLSVLR	480
QY	481	AMMYSGELKFEKRTSSAOVEGCVHSHLSYEKRLF	514
Dd	481	SMMYSSELKFEKRTMSPQIEGGVGHISHSYEKRLY	514

RESULT 12
ABC22269

ID	ABG22269	standard; Protein; 604 AA.
XX	AC	ABG22269;
XX	DT	18-FEB-2002 (first entry)
XX	DE	Novel human diagnostic protein #22260.
XX	KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
OS		Homo sapiens.
XX	PN	WO200175067-A2.
XX	PD	11-OCT-2001.
XX	PF	30-MAR-2001; 2001WO-US08631.
XX	PR	31-MAR-2000; 2000US-0540217.
XX	PR	23-AUG-2000; 2000US-0649167.
XX	PA	(HYSE-) HYSEQ INC.
XX	P1	Dzmanac RT, Liu C, Tang YT;
XX	DR	WPI; 2001-639362/73.
XX	DR	N-PSDB; AAS86456.
PT		New isolated polynucleotide and encoded polypeptides useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
PT		-
PS		Claim 20; SEQ ID No 52628; 103pp; English.
XX		
XX		The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
CC		Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC		
XX		
XX	Sequence	604 AA;
SQ		
QY	Query Match	81.8%; Score 2141.5; DB 22; length 604;
	Best Local Similarity	80.2%; Pred. No. 1.1e-200;
	Matches 413; Conservative	43; Mismatches 58; Indels 1; Gaps 1;
Db	1	MADYLIISGTSYVPDDGLTAQQLFNCGGDLTYNDFLILPGYIDFTADQVDLTSA
Db	90	MADYLIISGGTGYVPEDGLTAQQLFASADDLTYNDFLILPGFIDFIADVLTSA
QY	61	LKTPLVSSPMDTVEAGMAIAMALTGIGIFIHNCCTPEFOANEVRKVKEYEGFITDPV
Db	150	LKTPLVSSPMDTVEADMAIAMALMGIGIFIHNCCTPEFOANEVRKVNFEOGFITDPV
QY	121	LSPKDRVVDVFEAKARHGFCCGIPITDTGRMGSRVLVGISSRDIDFLKEEHDCFL

Db	210	LSPSHTVGDVLEGMKMRHGFSGIPITFTGTMGSKLVGIVTSRDIDFLAEKDHITLLSEVMT
QY	181	KREDLVVAPRSITLKEANEILORSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA
Db	270	PRIELVAVAPAGVTLKEANEILORSKKGKLPVNDCEDELVAIIARTDLKKS
QY	241	KKQLLCGAALGTHEDDKYRLDLAQAQVDVVLVLDSSQGSNIFQINMIKIKDKYPNLQV
Db	330	QPOLLCGAAVDTREEDKYRLDLTQAQVDVIVLSSQGSNSVQYARVLYFKQYPHLQVL
QY	301	GGNVVTAQAQKNLIDAGVDALRVGMSGSCICIIQEVLAACGRPOAT-AVYKYEYARRFGV
Db	390	GGNVVTAQAQKNLIDAGVDGLRVGMSGSCICITQEVMAACGRPOGTCVTRXAEYARRFGV
QY	360	PVIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDA
Db	450	PIADGGIQTGVGHVVKALALGASTVMGSLAATTEAPGEYFFSDGVRLLKKYRGMGLDA
QY	420	MDKHLSSQNRIFYSEADKIKVAQGVSGAVQDKGSIHKFVPLYIAGIQHSCQDIGAKSLTQV
Db	510	MEKSSSSQKRYFSEGDKKVIAQGVSGSIQDKGSIQKFVPLYIAGIQHSCQDIGARSLSVL
QY	480	RAMMYSGEIKFEKRTSSAQVEGCVHSLHSYEKRLF
Db	570	RSMYSGELKFEKRTMSPQIEGCVHGLHSYEKRLY
RESULT 13		
AAU99361		
ID	AAU99361	standard; Protein; 509 AA.
XX	AC	AAU99361;
XX	DT	07-OCT-2002 (first entry)
XX	DE	Human oxidoreductase 1 (OXR1) protein.
XX		
KW		Human; enzyme; oxidoreductase 1; OXR1; oxidation-reduction; aerobic metabolism; free radical; superoxide; hydroxyl ion; oxidation; reduction; oxidation potential; gene therapy; rheumatoid arthritis; inflammatory bowel disease; cell proliferation; psoriasis; lymphoma; cancer; Parkinson's disease; atherosclerosis; neurological disorder; epilepsy; Alzheimer's disease; myopathy; myasthenia gravis; periodic paralysis; mental disorder; SAD; seasonal affective disorder; amnesia; metabolic disorder; angina; Down's syndrome; muscular dystrophy; smooth muscle disorder; asthma; hypertension; incyte 72101285CD1.
OS		Homo sapiens.
XX		
PN		WO200250284-A2.
XX		
PD		27-JUN-2002.
XX		
PF		18-DEC-2001; 2001WO-US49131.
XX		
PR		21-DEC-2000; 2000US-257802P.
PR		18-JAN-2001; 2001US-262901P.
XX		
PA		(INCY-) INCYTE GENOMICS INC.
XX		
PI		Tribouley CM, Lee EA, Yao MG, Elliott VS, Yue H;
XX		
DR		WPI; 2002-528450/56.
DR		N-PSDB; ABK89032.
XX		
PT		New human oxidoreductase polypeptides and polynucleotides, useful for diagnosing, treating and preventing e.g. cell proliferative (e.g. arteriosclerosis), neurological (e.g. epilepsy), metabolic (e.g. hyperproliferemia) -
XX		
PS		Claim 1; Page 113-114; 119pp; English.
XX		

QY 121 LSPKDRVDFEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEHHDCFLEEIMT 180
Db 112 ----- 111
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db 112 ----- 111
QY 241 KKQLCGAAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 300
Db 112 -KTLGCGAAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 170
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITIQEVLACGRPQATAVYKYEYARRFGVP 360
Db 171 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAACGRPQATAVYKYSEYARRFGVP 230
QY 361 VIADGGIQNVGHITAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420
Db 231 VIADGGIQNVGHITAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 290
QY 421 DKHLSSQNRVFESEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIDIGAKSLTQVR 480
Db 291 DKHLSSQNRVFESEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIDIGAKSLTQVR 350
QY 481 AMMYSGELKFEKRTSSAQVEGGVHSLHSEYKRLF 514
Db 351 AMMYSGELKFEKRTSSAQVEGGVHSLHSEYKRLF 384

RESULT 15

AAE18179
ID AAE18179 standard: Protein: 385 AA.

XX AC AAE18179;

DT 07-MAY-2002 (first entry)

DE Human modified inosine 5'-monophosphate dehydrogenase (IMPDH) #10.

XX KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW therapy; enzyme.

XX OS Homo sapiens.
OS Synthetic.

XX PN WO200185952-A2.

XX PD 15-NOV-2001.

XX PF 10-MAY-2001; 2001WO-US15457.

XX PR 10-MAY-2000; 2000US-203448P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Krystek SR, Sheriff S, Wilmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;

XX DR WPI; 2002-164105/21.

PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies -

XX PS Claim 8; Page 130-131; 161pp; English.

CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or

CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other
CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the
CC management of cancer or other proliferative-type diseases, and in
CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is human modified IMPDH. This sequence comprises a substitute
CC tetra-peptide for the subdomain region of wild-type IMPDH.

XX SQ Sequence 385 AA;

Query Match 71.1%; Score 1861.5; DB 23; Length 385;
Best Local Similarity 74.3%; Pred. No. 1.5e-173;
Matches 382; Conservative 0; Mismatches 3; Indels 129; Gaps 2;

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Db 111 -SP----- 112

QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240

Db 113 ----- 112

QY 241 KKQLCGAAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 300

Db 113 -TQLGCGAAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 171

QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITIQEVLACGRPQATAVYKYEYARRFGVP 360

Db 172 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAACGRPQATAVYKYSEYARRFGVP 231

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Db 352 AMMYSGELKFEKRTSSAQVEGGVHSLHSEYKRLF 385

Search completed: February 13, 2003, 04:50:19
Job time : 89 secs

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GenCore version 5.1.3
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Run on: February 12, 2003, 15:12:14 ; Search time 1203 seconds
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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2	1635.6	98.9	1642	6	AR141889	AR141889 Sequence
3	1635.6	98.9	1642	6	I06570	I06570 Sequence 1
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5	1616.6	97.7	1648	9	BC012840	BC012840 Homo sapi
6	1614.6	97.6	1655	9	BC015567	BC015567 Homo sapi
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8	1326.6	80.2	1707	10	MUSIMPDA	M33934 Mouse IMP d
9	1322.2	79.9	1680	10	BC010314	BC010314 Mus muscu
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45	761	46.0	172237	2	AC131389	AC131389 Homo sapi

ALIGNMENTS

RESULT 1	
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LOCUS	HUMIMP
DEFINITION	Human inosine-5'-monophosphate dehydrogenase (IMP) mRNA, complete cds.
ACCESSION	J04208
VERSION	J04208.1 GI:186391
KEYWORDS	Inosine-5'-monophosphate dehydrogenase.
SOURCE	Human peripheral blood leukocyte, cDNA to mRNA, clone HIMP.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1654)
TITLE	Collart,F.R. and Huberman,E. Cloning and sequence analysis of the human and Chinese hamster

Pred. No. is the number of results predicted by chance to have a

JOURNAL J. Biol. Chem. 263 (30), 15769-15772 (1988)
MEDLINE 89008491
PUBMED 2902093

COMMENT Draft entry and computer-readable sequence for [1] kindly provided by F.R.Collart, 22-AUG-1988.

FEATURES
source location/Qualifiers

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/db_xref="taxon:9606"
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/translation="MADYLLISGTSYVPDDGLTAQQLFNCGDGLTYNDLILPGYIDF
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RDIDFLKEEHDCLFLEIMTRREDLVVAPRSITLKEANEILORSKKGKLPVNEDEL
VAIARTDLKKNRDIPLASKDAKKQLLGAALGTHEDDKYRLDLLAQVDVYVLLDSS
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BASE COUNT 415 a 418 c 451 g 370 t
ORIGIN 45 bp upstream of Ball site.

Query Match 99.6% ; Score 1647.6 ; DB 9 ; Length 1654 ;
Best Local Similarity 99.8% ; Pred. No. 0 ;
Matches 1650 ; Conservative 0 ; Mismatches 4 ; Indels 0 ; Gaps 0 ;

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DEFINITION Sequence 1 from patent US 6147194.
ACCESSION ARI41889
VERSION ARI41889.1 GI:15101405
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1642)
AUTHORS Collart, F.R. and Huberman, E.
TITLE Eukaryotic IMPDH polynucleotide and antibody compositions
JOURNAL Patent: US 6147194-A 1 14-NOV-2000;
FEATURES
source 1. 1642
BASE COUNT 411 a 416 c 449 g 366 t
ORIGIN

Query Match 98.9%; Score 1635.6; DB 6; Length 1642;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from Patent WO 9001545.
ACCESSION 106570
VERSION 106570.1 GI:589653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
REFERENCE      1 (bases 1 to 1642)
AUTHORS        Collart,F.R. and Huberman,E.
TITLE          METHOD AND MATERIALS RELATING TO IMPDH AND GMP PRODUCTION
JOURNAL        Patent: WO 9001545-A 1 22-FEB-1990;
FEATURES       Location/Qualifiers
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ORIGIN
Query Match   98.9%; Score 1635.6; DB 6; Length 1642;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GGGGGTCTCGGAGACACGGCGGTGTCTGTGTTGGCCATGGCCGACTACCTGATTA 66
Db 1 GGGGGTCTCGGAGACACGGCGGTGTCTGTGTTGGCCATGGCCGACTACCTGATTA 60

QY 67 GTGGGGCAGCTCCTACGTGCCAGACGAGCTCACAGCAGCAGCTCTTCAACTGG 126
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RESULT 4
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DEFINITION Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone
ACCESSION BC006124
VERSION    BC006124
KEYWORDS   MGC.13021 IMAGE:3545693, mRNA, complete cds.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens.
REFERENCE  1 (bases 1 to 1663)
AUTHORS    Strausberg,R.
TITLE      Direct Submission
JOURNAL    Submitted (02-APR-2001) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer
           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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REMARK
COMMENT

USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaro Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsch, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 18 Row: f Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Genomescan gene prediction.

FEATURES
source

1. 1663
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CDS

BASE COUNT 436 a 412 c 448 g 367 t
ORIGIN
Query Match 98.1%; Score 1622.6; DB 9; Length 1663;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 5
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LOCUS
DEFINITION Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone
ACCESSION MGC:9332 IMAGE:3447994, mRNA, complete cds.
VERSION BC012840.1 GI:15277479
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1648)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Huliyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAK Plate: 12 Row: a Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES
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BASE COUNT 428 a 409 c 445 g 366 t
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Query Match 97.7%; Score 1616.6; DB 9; Length 1648;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1622; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 6
BC015567
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DEFINITION Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone
ACCESSION BC015567
VERSION BC015567.1 GI:15990411
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantrop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAL Plate: 30 Row: 3 Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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/clone_id="NIH_MGC_48"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
41. 1585
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/db_xref="GI:15990412"
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BASE COUNT 430 a 410 c 450 g 365 t
ORIGIN

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Matches 1620; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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LOCUS 225727 bp DNA linear HTG 30-JUL-2002
DEFINITION Mus musculus chromosome UNK clone RP24-455L10, WORKING DRAFT
AC122514
AC122514.2 GI:22004610
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLLTOP.
SOURCE
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 225727)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
JOURNAL
REFERENCE
AUTHORS 2 (bases 1 to 225727)
McPherson,J.D. and Waterston,R.H.
Direct Submission
JOURNAL
TITLE Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 225727)
McPherson,J.D. and Waterston,R.H.
Direct Submission
JOURNAL
TITLE Submitted (30-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT On Jul 30, 2002 this sequence version replaced gi:21105978.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0455L10

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 224286 bases at least Q40
Consensus quality: 224589 bases at least Q30
Consensus quality: 224737 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 225627; sum-of-ontigs
Quality coverage: 15.05 in Q20 bases; agarose-fp
Quality coverage: 11.65 in Q20 bases; sum-of-ontigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 53314: contig of 53314 bp in length
* 53315 53414: gap of unknown length
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Best Local Similarity 88.1%; Pred. No. 0;
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RESULT 8

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ACCESSION M33934
VERSION M33934.1 GI:198393
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SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1707)
AUTHORS Tiedeman,A.A. and Smith,J.M.
TITLE Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase
JOURNAL Gene 97 (2), 289-293 (1991)
MEDLINE 91153661
PUBMED 1671845
COMMENT Draft entry and computer-readable sequence for [Unpublished (1990)]
        kindly submitted
        by J.M.Smith 27-APR-1990.
        Author address:
            Dr. J.M. Smith
            Seattle Biomedical Research Institute
            4 Nickerson St.
            Seattle, WA 98109.

FEATURES
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BASE COUNT      457 a      408 c      451 g      391 t
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Query Match      80.2%; Score 1326.6; DB 10; length 1707;
Best Local Similarity 87.9%; Pred. No. 0;
Matches 1446; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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QY	1507	AGCTTAAGTTTGACAGAGAAGACGTCCTCAGCCCAAGGTGGAAGGTGGCGTCCATAGCCTCC	1566
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QY	1567	ATTGCGTATGAGAAGCGGCTTTTCTGAAAAGGGATCCAGCAACCTCCTTGGTTTCTTTT	1626
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[illegible]

Query Match	79.98;	Score 1322.2;	DB 10;	length 1680;
Best Local Similarity	88.28;	Pred. No. 0;		
Matches 1438; Conservative	0;	Mismatches 193;	Indels 0;	Gaps 0

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	
Email: cgabs-remail.nih.gov	
Tissue Procurement: Gilbert Smith, Ph.D.	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center	
Center code: BCM-HGSC	
Web site: http://www.hgsc.bcm.tmc.edu/cdna/	
Contact: amg@bcm.tmc.edu	
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
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34. .1578	

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QY	75	ACGTCTACGTGCGCCAGACGACGGACTCACAGCACAGCAGCTCTTCACTGCGGAGACGGC	134
Db	61	ACCTCTTACGTGCCGGAGCAGCGGGCTCACAGCGCAGCAGCTCTTCACTGCGGGGACGGC	120
QY	135	CTCACCTACATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACCAAGTg	194
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QY	195	GACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTTCTCTCC	254
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QY	315	TTCATCCACCCACAACCTGTACACCTGAATTCAGGCCAATGAAGTTCGGAAGTGAAGAAA	374
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QY	375	TATGAACAGGGAATTCATCACAGACCCGTGGTCTCAGGCCCAAGGATCGCGTGGGGAT	434
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ACCESSION ARI41890					
VERSION ARI41890.1 GI:15101406					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unknown.					
REFERENCE 1 (bases 1 to 1620)					

AUTHORS		Collart, F.R. and Huberman, E.									
TITLE		Eukaryotic IMPDH polynucleotide and antibody compositions									
JOURNAL		Patent: US 6147194-A 2 14-NOV-2000;									
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QY	263	AGTCACAGAGGCTGGGATGGCCATAGCAATGGCGCTTACAGGCGGTATTGGCTCATCCA	322								
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QY	383	GGGATTCATACAGACCCCTGTGTCTCAGCCCCAAGGATCGCGTGGGATGTTTTGA	442								
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ACCESSION	106572						
VERSION	106572.1						
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ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1620)						
AUTHORS	Collart, F.R. and Huberman, E.						
TITLE	METHOD AND MATERIALS RELATING TO IMPDH AND GME						
JOURNAL	Patent: WO 9001545-A 3 22-FEB-1990;						
FEATURES	Location/Qualifiers						
BASE COUNT	423 a 369 c 421 g 407 t						
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QY	443	GGCCAAAGGCCCATGGTTTCTGCGGTATCCCAATCACAGACACAGCGCGATGGGAG	502	
Db	421	AGCCAAAGCCAGGCATGGCTTCTGTGTATCCCATCACAGATACAGCGCGATGGGAG	480	
QY	503	CGCTTGTGGGCATCATCTCTCCAGGACATTGATTTCTCAAGAGAGGAAACATGA	562	
Db	481	TCGACTGTGGGCATCATTTCTTCAAGGATATTGATTTCTCAAGAGAGGAAACATGA	540	
QY	563	CTGTTTCTTGAAGAGATTAATGACAAAGAGGGAAGACTTGTGTAGCCCCCGCAGCAT	622	
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QY	623	CACACTGAAGCAGGCAAAATGAATTTCTGAGCGCAGCAAGAGGAAAGTTGCCATTGT	682	
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RESULT 12			
CRUIP			
LOCUS	CRUIP	1614 bp	mRNA
DEFINITION	Chinese hamster inosine-5'-monophosphate dehydrogenase (IMP) mRNA,		
	complete cds.		
ACCESSION	J04209		
VERSION	J04209.1	GI:191119	
KEYWORDS	inosine-5'-monophosphate dehydrogenase.		
SOURCE	Chinese hamster cell line E29Pro+, clone CIMP.		
ORGANISM	Cricetulus griseus		
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	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;		
	Cricetulus.		
REFERENCE	1 (bases 1 to 1614)		
AUTHORS	Collart,F.R. and Huberman,E.		
TITLE	Cloning and sequence analysis of the human and Chinese hamster		
JOURNAL	inosine-5'-monophosphate dehydrogenase cDNAs		
MEDLINE	J. Biol. Chem. 263 (30), 15769-15772 (1988)		
PUBMED	89008491		
COMMENT	2902093		
	Draft entry and computer-readable sequence for [1] kindly provided		
	by F.Collart, 07-SEPT-1988.		
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ORIGIN
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QY	83	CGTGCCAGACGACGAGACTCACAGCACAGCAGCTCTTCAACTGCGGAGACGGCCTCACCTA	142	
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QY	1403	AATCCAAATTTGTCCCTTACCTGATTTGCTGGCATCCAAACATCATCCAGGACATTGG	1462
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QY	1463	TGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGAGCTTAAAGTTGAGAA	1522
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QY	1583	GCTTTTCTGAAAAGGATCCAGCACACCTCCTCGGTTTTTTTTCAA	1629
Db	1561	GCTTTTCTGAAAAGAGATCCAGTATATGCCCTTGAATTTTTCATTA	1607
RESULT 13			
MUSIMPDA			
LOCUS	MUSIMPDA	1545 bp	mRNA
DEFINITION	Mus musculus IMP dehydrogenase (IMP) mRNA, complete cds.		
ACCESSION	M98333		
VERSION	M98333.1	GI:425157	
KEYWORDS	IMP dehydrogenase.		
SOURCE	Mus musculus brain cDNA to mRNA.		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 1545)		

AUTHORS	Lightfoot,T. and Snyder,F.F.									
TITLE	Gene amplification and dual point mutations of mouse IMP dehydrogenase associated with cellular resistance to mycophenolic acid									
JOURNAL	Biochim. Biophys. Acta 1217 (2), 156-162 (1994)									
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QY	108	CAGCAGCTCTTCAACTGGGAGACGGGCTCACCTACAATGACTTTCTCATTTCTCCCTGGG								167
Db	61	CAGCAGCTCTTCAACTGGCGGAGACGGGCTCACCTACAATGATTTTCTCATTTCTCTGGG								120
QY	168	TACATCGACTTCACTGCAGACCAAGTGGACCTGACTTCTGCTCTGACCAAGAAATCACT								227
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QY	228	CTTAAGACCCCACTGTTTCTCTCCATGACACAGTCAACAGAGGCTGGATGGCCATA								287
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LOCUS			
DEFINITION			
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ACCESSION			
AK054667			
VERSION			
AK054667.1 GI:16549257			
KEYWORDS			
oligo capping; fis (full insert sequence).			
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ORGANISM			
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REFERENCE			
AUTHORS			
1 Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuko,Y., Nagai,K. and Isogai,T.			
TITLE			
NEDO human cDNA sequencing project			
JOURNAL			
unpublished			
REFERENCE			
2 (bases 1 to 2479)			
Isogai,T., Otsuki,T. and Sugiyama,T.			
AUTHORS			
Direct Submission			
JOURNAL			
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)			
COMMENT			
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.			
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QY	167	GTACATGCACTTCACTGCAGACCAAGGTGACCTGACTTCTGCTCTGACCAAGAAATCAC	226
Db	348	ATTCAATGACTTCAATGATGATGAGGTGACCTGACCTCAGCCCTGACCCGGAAGATCAC	407
QY	227	TCTTAAGACCCCACTGGTTTCTCTCCATGGACACAGTCAAGAGGCTGGATGGCCAT	286
Db	408	GCTGAAGACGCCACTGATCTCTCTCCCATGACACTGTGACAGAGGCTGACATGGCCAT	467

QY	287	AGCAATGGCGCTTACAGCGCGTATTGGCTTCATCCACCACACTGTAC	CCCTGAATTCCA	346
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QY	467	CGGTATCCCAATCACACACACAGCGCCGATGGGAGCGCCCTTGGTGGG	ATCATCTCCTC	526
Db	648	TGGCATCCCATCTACTGAGACGGGCAACCATGGGACGACAAGCTGTTGGG	ATCGTCACTTC	707
QY	527	CAGGACATTGATTTTCTCAAGAGGAGGAACATGACTGTTTCTTGA	GAGATTAATGAC	586
Db	708	CCGAGACATCGACTTCTTCTGCTGAGAAGGACCACACCCTCCTCAG	GAGGTGATGAC	767
QY	587	AAAGAGGAGAGACTTGGTGGTAGCCCCCGCAGCATCACACTGAAGGA	GCAAAATGAAT	646
Db	768	GCCAAGGATTGAACTGGTGGCTCCAGCAGGTGTGACGTTGAAGA	GCAAAATGAGAT	827
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Db	948	CCAGAAGCAGCTCCTCTGTGGGGCAGCTGTGGGCGACCCCTGAGGATGA	CAAAATACCGTCT	1007
QY	827	GGACTTGTCTGCCCGCAGCGCTGGTGTGATGTAGTGGTTTGGACTCTTC	CCAGGAAATTC	886
Db	1008	GGACCTGCTCACCCAGCGCGGCGTGCAGCTCATAGTCTTGGACTCGTC	CAAGGGAATTC	1067
QY	887	CATCTTCCAGATCAATATGATCAAGTACATCAAGACAATATACCCTAA	CTCCAAGTCAT	946
Db	1068	GGTGTATCAGATCGCCATGTGTGATTTACATCAAAAGAAATACCCCA	CTCCAAGTGTAT	1127
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QY	1007	CCTGCGGGTGGCATGGGAAGTGGCTCCATCTGCAATTATCCAGGAAGT	CTGCGCTGTGG	1066
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QY	1127	GCTCATTTGCTGATGAGGAATCCAAATGTGGGCTCATATTGGGAAAGC	CTTGGCCCTTGG	1186
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QY	1187	GGCCTCCACAGTCATGATGGGCTCTCTCTGCTGGCTGCCACCCTAGAGGC	CCCTGGTGAATA	1246
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RESULT	15
LOCUS	BC033622
DEFINITION	BC033622 2520 bp mRNA linear PRI 08-JUL-2002
ACCESSION	Homo sapiens, IMP (inosine monophosphate) dehydrogenase 1, clone MGC:40351 IMAGE:5210847, mRNA, complete cds.
VERSION	BC033622
KEYWORDS	BC033622.1 GI:21706906
SOURCE	MGC.
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2520)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2002) National Institutes of Health, Mammalian

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q. L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantrilop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
Series: IRAK Plate: 64 Row: j Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504686.

FEATURES

Location/Qualifiers

source

CDS

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Query Match	58.3%	Score 963.6;	DB 9;	Length 2520;
Best Local Similarity	76.5%;	Pred. No. 5.1e-250;		
Matches 1182; Conservative	0;	Mismatches 364;	Indels 0;	Gaps 0;

[illegible]

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1321.8	79.9	1620	3	US-08-925-230-2	Sequence 2, Appli
3	420.6	25.4	675	4	US-09-328-111-844	Sequence 844, App
4	410.2	24.8	3616	4	US-09-212-247C-7	Sequence 7, Appli
5	285.8	17.3	393	3	US-08-925-230-5	Sequence 5, Appli
6	285.8	17.3	393	3	US-08-925-230-6	Sequence 6, Appli
7	275.8	16.7	344	3	US-08-925-230-3	Sequence 3, Appli
8	275.8	16.7	344	3	US-08-925-230-4	Sequence 4, Appli
9	226.2	13.7	3531	1	US-08-629-600-1	Sequence 1, Appli
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12	154.6	9.3	5884	4	US-09-221-017B-497	Sequence 497, App
13	118.4	7.2	1653	4	US-08-961-527-329	Sequence 329, App
14	81.6	4.9	1843	1	US-08-774-169-2	Sequence 2, Appli
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20	35.8	2.2	2353	1	US-08-328-322-11	Sequence 11, Appl
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22	35	2.1	7326	4	US-09-514-247A-7	Sequence 7, Appli
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ALIGNMENTS

RESULT 1
US-08-925-230-1
Sequence 1, Application US/08925230
Patent No. 6147194
GENERAL INFORMATION:
APPLICANT: Collart, Frank
APPLICANT: Huberman, Eliezer
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
NUMBER OF INVENTIONS: 8
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,230
FILING DATE: September 8, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,665,583
FILING DATE: 12-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-925-230-1

Query Match 98.9%; Score 1635.6; DB 3; Length 1642;
Best Local Similarity 99.8%; Pred.No. 0;
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RESULT 2
US-08-925-230-2
: Sequence 2, Application US/08925230
: Patent No. 6147194
: GENERAL INFORMATION:
: APPLICANT: Collart, Frank
: APPLICANT: Huberman, Eliezer
: TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
: TITLE OF INVENTION: AND GMP PRODUCTION
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/925,230
: FILING DATE: September 8, 1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 5,665,583
: FILING DATE: 12-AUG-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Wilson, Mark B.
: REGISTRATION NUMBER: 37,259
: REFERENCE/DOCKET NUMBER: ARCD:274
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-925-230-2

Query Match 79.9%; Score 1321.8; DB 3; Length 1620;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1442; Conservative 0; Mismatches 177; Indels 4; Gaps 1;

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QY	1103	GTATGACGGCCTTGTGGTGTCCGGTCAATTGCTGATGAGGAATCCAAATGTGGTCA	1162
Db	1081	GTATGCTGGCGCTTGTGGTGTCTGTTATTGCTGATGAGGAATCCAAATGTGGTCA	1140
QY	1163	TATTGGGAAAGCCTTGGCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCGCTGC	1222
Db	1141	TATTGCCAAAGCTTTGGCTTTGGAGCTTCTACAGTCATGATGGGCTCTCTTGGCTGC	1200
QY	1223	CACCACTGAGGCCCTGTGTAATCTCTTTCCGATGGATCCGGCTAAGAAATATCG	1282
Db	1201	CACCAACGAAAGCCCTGTGTAATCTCTTCTCAGATGGATCCGGCTAAGAAATATCG	1260
QY	1283	CGTATGGGTTCTCTGATGCCATGGACAAGCACCTCAGCAGCCAGAACAGATATTTCAG	1342
Db	1261	TGATATGGGTTCTCTGATGCCATGGACAAGCATCTCAGCAGCCAGAACAGATATTTCAG	1320
QY	1343	TGAAGCTGACAAATCAAAAGTGGCCAGGAGTGTCTGTGTGTGACAGCAAAAGGTC	1402
Db	1321	TGAAGCTGACAAATCAAAAGTGGCCAGGAGTGTCTGTGTGTGACAGCAAAAGGTC	1380
QY	1403	AATCAACAAATTTGTCCCTTACCTGATTTGCTGGCATTCACAACATCATGCCAGCATTCG	1462
Db	1381	TATCCAAAGTTGCTGCCCTTATTTGATTTGCTGGCATTCACAACATCATGCCAGCATTCG	1440
QY	1463	TGCCAAGACTTGACCCAAAGTCCGAGCCATGATGTACTGTGGAGACTTAAAGTTGAGAA	1522
Db	1441	TGCCAAGACTTTAAACCAAGTCAAGCCATGATGTACTGTGGAGACTTAAAGTTGAGAA	1500
QY	1523	GAGAAGTCTCAGCCAGGTGGAAGGTGGCTCATAGCCCTCAATTCGTATGAGAAGCG	1582
Db	1501	GAGAAGTCTCAGCTCAGGTGGAAGGTGGTGCACAGCCTTCATTCGTATGAGAAGCG	1560
QY	1583	GCTTTCTGAAAAGGATCCAGCACACCTCCTCGGTTTTTTTCAATAAAGTTTAGAA	1642
Db	1561	GCTTTCTGAAAAGAGATCCAGTATATATGCTTGAATTTTCAATAAAGTTTAGAA	1616
QY	1643	AGA 1645	
Db	1617	AAA 1619	

RESULT 3
US-09-328-111-844
; Sequence 844, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)

Db	1928	GTCAATTGCTGGCAACGTCGTGTCACCAGAGAGCAGCGCTGGCCAGCTTGATCCACGCCGGCGCA	1987
OY	1002	GATGCCCTGCGGGGTGGGATGGGAAGTGGCTCCATCTGCATTATCCAGCAAGTGTGCCC	1061
Db	1988	GACGGGTTCGTATCGGTATGGGCTCTGGCTCCATCTGATCACTCAGCAAGTGTATGGCC	2047
OY	1062	TGTGGCGGCGCCCAAGCAACAGCAGTGTACAAGGTGTATGAGTATGCAATGGCGCTTGGT	1121
Db	2048	TGTGGTAGACCACAGGCTAACCGCTGTCTACACAGCTCACGCCAGTTGGCCACCGAGTTGGT	2107
OY	1122	GTTCGGGTCAATTGCTGATCGAGGAATCCAAATGTGGGTATATTGGCAAGCCTTGGCC	1181
Db	2108	GTGCCATGATATTGCTGACGGTGGTGTCCAGAACATCGGGCACATTACCAAGCTATCGCT	2167
OY	1182	CTTGGGGCTCCACAGTCATGATGGGCTCTCTCTGGCTGCCACCACCTCAGGCCCTGGT	1241
Db	2168	CTTGGCGCGTCCACCGCTCATGATGGCGGTATGCTGGCAGGCACTACACAGTCTCCAGGC	2227
OY	1242	GAATACTCTTTTCCGATGGGATCCGGCTAAAGAAATATCGCGGTATGCGTCTCTCGAT	1301
Db	2228	GAGTACTTCTTCAGGGACGGGAAGAGACTGAAGACTACAGAGGTATGCGCTCCATCGAC	2287
OY	1302	GCCATGGACAAGCACCCTCAGCAGCCAGAA-----CAGATATCTCAGTGAAGCT	1349
Db	2288	GCCATGCAAAAAGACTGATGTCAAGGGTAACGCCGCTAACCCTCCGTTACTCTCTGAGTCT	2347
OY	1350	GACAAATCAAAAGTGGCCCGAGGAGTGTCTGGTGTCTGACAGACAACACGCTCAATCCAC	1409
Db	2234	GACAAGGTTCTGTCGCTCAGGGTGTACTGGTCTCTGTGATCGACAACGCTCCATCAAG	2407
OY	1410	AAATTTGTCCCTTACCTGATTTGCTGGCATCCAACACTCATGCCCAGGACATTTGGTGGCAAG	1469
Db	2408	AAGTACATTTCCATATCTCTACAAATGCTCTACAGCACTCTGCCCAGGATATCCGTTGTCCG	2467
OY	1470	AGCTTGACCCAGTCCGAGCCCATGATGTACTCTGGGAGCTTAAGTTTACAGACGACAAG	1529
Db	2468	TCTCTAGTGGAGTTTCAGAGAGAAGGTGAGACTCTGGCTCGGTACAGATTTTACGTTACGAAC	2527
OY	1530	TCCTCAGCCAGGTGCAAGGTGGCGTCCATAGCCTTCATTTGATATGACCAAGCGGCTTTT	1588
Db	2528	CCATCTGCCCAGTTGAGGGGTGGTGTGCACAACCTTCCACTCCTACGACAAGCGCCTATT	2586

RESULT 5
US-08-925-230-5/C
Sequence 5, Application US/08925230
Patent No. 6147194
GENERAL INFORMATION:
APPLICANT: Collart, Frank
APPLICANT: Huberman, Eliezer
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
TITLE OF INVENTION: AND GMP PRODUCTION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,230
FILING DATE: September 8, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,665,583
FILING DATE: 12-AUG-1988
ATTORNEY/AGENT INFORMATION:

```

; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..393
; OTHER INFORMATION: /note="This sequence is the top
; OTHER INFORMATION: strand of a double stranded sequence. The sequence immedi
; OTHER INFORMATION: following is the bottom strand of the double stranded sequ

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Query Match	17.3%;	Score 285.8;	DB 3;	Length 393;
Best Local Similarity	89.6%;	Pred. No. 1e-78;		
Matches 352;	Conservative 0;	Mismatches 37;	Indels 4;	Gaps
QY 771	AAACAGCTGCTGTGTGGGCGAGCCATTGGCAGCTCATG-AGGATGACAAGTATAGGCTGCA	829		
Db 393	AAAGCAACTGCTGTGT-GGGCAGCCATTGGCAGCTCATGAGGATGACAAGTATAGGCT-GA	336		
QY 830	CTTGCTCGCCAGGCTGTGTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCAT	889		
Db 335	CTTACTGGCCCTTGCTGTGTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCAT	276		
QY 890	CTTCCAGATCATATATGATTCAGTACATCAAGACAATAACCCTAATCTCCAGTCAATTGG	949		
Db 275	CTTCCAATCATATATGATTCACAATACATCAAGGAGAGAGATATCCAGTCTACAGTCAATTGG	216		
QY 950	AGGCAATGTGCTCA-CTGCTGCCCAAGGCCAAGACCTTCATTGATGCAGGTGTGATGCC	1008		
Db 215	AGGCAATGTACTACCTGCTGCCGAAGCCAGAACCCTCATAGATGCAGGTGTAGATGCTT	156		
QY 1009	TGCGGGTGGGCATGGGGAAGTGGCTCCATCTGCATTATTCAGGGAAGTGTGGCCTGTGGCC	1068		
Db 155	TGCGAGTGGGCATGGGGAAGTGGTTCCATCTGCATCACCCAGGAAGTGTGGCCTGTGGCC	96		
QY 1069	GGCCCCAAGCAACAGCAGTGTACAAGGTGTATAGATGCAACGGGCTTTGGTGTTCGG	1128		
Db 95	GGCCCCAAGCCACAGCAGTGTACAAGGTCTGTAGATGCCCCGTGCTTGGTGTTCCTG	36		
QY 1129	TCATTGCTGATGAGGAATCCAAATGTGGGTC	1161		
Db 35	TTATTGCTGATGAGGAATCCAAATGTGGGTC	3		

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RESULT 6
US-08-925-230-6
; Sequence 6, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; APPLICANT: Huberman, Eliezer
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; TITLE OF INVENTION: AND GMP PRODUCTION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;

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; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; APPLICANT: Huberman, Eliezer
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; TITLE OF INVENTION: AND GMP PRODUCTION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..344
; OTHER INFORMATION: /note= "This sequence is the bottom
; strand of a double stranded sequence, read from 5' to 3'. The
; OTHER INFORMATION: top strand with which it belongs is the sequence immediately
; preceding it in this listing."
US-08-925-230-4

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	Query Match	16.7%;	Score 275.8;	DB 3;	Length 344;	
	Best Local Similarity	87.8%;	Pred. No. 1.2e-75;			
	Matches 301;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0;	
QY	412 GCCCCAAGGATCGCGTCGGGGATGTTTGTGAGGCCAAGGCCCGGCATGCTTCTGCGGTA					471
Db	343 GCCCCAAGGATCGTGACCGCATGTTTTGAGGCCAAAGCCAGGCATCGCTTCTGTGTA					284
QY	472 TCCCAATCACAGACACAGGCCCGGATGGGAGCCGCTTGGTGCGCATCATTCTCTCCAGG					531
Db	283 TCCC CATCACAGATACAGGCCCGGATGGGAGTGCATTGCTGGG CATCATCTCTCTCAAGG					224
QY	532 ACATTGATTTTCTCAAAGAGGAGAACAATGACTGTTCTTGGAAAGATTAATGACAAAGA					591
Db	223 ACATTGATTTCTCTCAAGGAGGAAGAGACATGACC GGTTCTTGGAAAGATTCATGACTAGA					164
QY	592 GGGAAGACTTGGTGTAGCCCCCCCCCGAGCATCACACTGAAGGAGCAATGA AATTCTGC					651
Db	163 GGGAAGATTTGGTGTCTGCC CCCCCCTGCCGGCGTCACTCTGAAGAAGGCCAATGAGATTCTGC					104
QY	652 AGCGCAGCAGAAGGGAAGTTGCCCATTTGTA AATGAAGATGATGAGTTGTGGCCATCA					711
Db	103 AGCGAAGTAAAAAAGGGAAGTTGCCCATTTGTGAATGA AATGATGAGDTGGTAGCCATCA					44
QY	712 TTGCCCCGACAGACCTTGGAAGAAGATCGG GACTATCCCACTAGC 754					

Db 43 TTGCCCGACAGACCTTAAGAGAATCGTGATTACCCCTGGC 1

RESULT 9
US-08-629-600-1
; Sequence 1, Application US/08629600

GENERAL INFORMATION

GENERAL INFORMATION:

APPLICANT: NORIEGA, Fernand
APPLICANT: LEVINE, Myron M.

TITLE OF INVENTION: GUA MUTANTS OF SHIGELLA
TITLE OF INVENTION: AND VACCINES CONTAINING THE SAME

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS.

ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 3100 Pennsylvania Avenue N.W. Suite 900
CITY: Washington, D.C. 20037

STATE: Pennsylvania AVEUE, N.W., SUITE 800
CITY: Washington, D.C.

STATE: D.C.
COUNTRY: U.S.A.

ZIP: 2003/
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6229,600

FILING DATE: 9-APR-1996
CLASSIFICATION: A24

ATTORNEY/AGENT INFORMATION:
NAME: KTH Gordon

NAME: NII, GILGON
REGISTRATION NUMBER: 30,764
REFERENCE DOCUMENT NUMBER: 5755

REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
ATTENTION: 603-235-7550

TELEPHONE: (202) 293-7066
TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

LENGTH: 3531 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO

US-08-629-600-1

ANIL SENSE
US-08-629-600-1

Query Match	13.7%;	Score 226.2;	DB 1;	Length 3531;
Best Local Similarity	49.5%;	Pred. No. 1.1e-59;		
Matches 650;	Conservative 0;	Mismatches 648;	Indels 15;	Gaps 2;

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Db	388	TACTGCTGACCTCAGCACCCAGCTGACGAAAACTATTGCTGTAATATCCCTATGCTTTC	447
QY	248	CTCTCCCATGACACACAGTCACAGAGCGCTGGGATGGCCATAGCAATGGCGCTTACAGCGG	307
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QY	308	TATTGGCTTCATCCACCACCAACTGTACACCTGAATTCACAGGCCAATGAAGTTCCGAAGT	367
Db	508	TATCGGCTTATTCACCAAAAAACATGTTCATTGGAACGCCAGCGAGAAGAAGTTCGCCGTGT	567
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QY	428	GCGGATGTTTTTGAGGGCCAAGGCCCGCATGTGTTTCTGGGCTATCCCAATCACAGACAC	487

Db 628 GCCGGAAGTGAAGAAGTACCGGAGCGGTAACGGTTTGGGGGCTATCCGGTCTTACCGA 687
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QY 1028 TGGCTCCATCTGCATTATCCAGAAAGTGGCTGGCTGTGGCGGCCCAAGCAACAGCAGT 1087
Db 1213 TGGCTCTATCTGTACAACCTGATATCGTACTGGCGTGGTTCGCGCAGATTACCGCTGT 1272
QY 1088 GTACAAGTGTATGAGTATGACAGCGCGCTTGGTGTCCGGTCAATTGCTGATGAGGAAT 1147
Db 1273 TGCTGACGCAGTAGAAGCCCTGGAAGGCAACCGGTATTCGGTTATCGGTATGGCGGTAT 1332
QY 1148 CCAAAATGTGGGTCAATATTGCGAAAGCCTTGGCCCTTGGGGCCTCCACAGTCATGATGGG 1207
Db 1333 TCGCTTCTCCGGCGACATCGCCAAAGCTATCGCCGCTGGCGCAAGCGGTGATGGTAGG 1392
QY 1208 CTCTCTCTGGCTGCCACCACTGAGGCGCCCTGGTGAATACTTCTTTTCCGATGGGATCCG 1267
Db 1393 TTCCATGCTGGCGGGTACTGAAGAATCTCGGGGTGAATCGAATCTTACCAGGGCGCTTC 1452
QY 1268 GCTAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCAACCTCAGCAGCCA 1327
Db 1453 TTACAATCTTACCCTGGTATGGGTTCCCTGGGCGCGATGTCCAAAGGTTCTCTGACCG 1512
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Db 1513 TTATTTCAGAGCGATTAACGCTGCCGACAAACTGGTGCCGGAAGGTATCGAAAGTGGCGT 1572
QY 1388 GCAGACAAGGCTCAATCCACAATTTGCCCTTACCTGATTTGCTGGCATCC 1440
Db 1573 AGCCTATAAAGTCCGCTGAAGAGATCAATTCACACGACAGATGGCGCGCTGC 1625

RESULT 10
US-09-076-761-1
; Sequence 1, Application US/09076761
; Patent No. 6190669
; GENERAL INFORMATION:

APPLICANT: NORIEGA, Fernando
APPLICANT: SZEIN, Marcelo B.
APPLICANT: LEVINE, Myron M.
TITLE OF INVENTION: ATTENUATED MUTANTS OF SALMONELLA
TITLE OF INVENTION: WHICH CONSTITUTIVELY EXPRESS THE
TITLE OF INVENTION: VI ANTIGEN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
City: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,761
FILING DATE: 13-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-7140
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-076-761-1

Query Match 13.7%; Score 226.2; DB 4; Length 3531;
Best Local Similarity 49.5%; Pred. No. 1.1e-59;
Matches 650; Conservative 0; Mismatches 648; Indels 15; Gaps 2;
QY 128 AGACGGCTCACCTACATGACTTTCTCAFTTCTCCCTGGGTACATCGACTTCACGTGACAGA 187
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Db 388 TACTGCTGACCTCAGACACCCAGCTGACGAANAATATTGCTGAATATCCCTATGCTTTC 447
QY 248 CTCTCCCATGACACACAGTCACAGAGGCTGGGATGGCCATAGCAATGGCGCTTACAGGCGG 307
Db 448 CGCAGCAATGGATACCGTAAACGGAAGCGCGCTGGCTATTTGCTCTGGCTCAGGAAGGCGG 507
QY 308 TATTGGCTTCATCCACCACTGTACACCTGAATTCAGAGCCCAATGAAGTTCGGAAGT 367
Db 508 TATCGCTTTATCCACAAAACATGTCCATTGAACGCCAGGCAAGAAGTTGCGCGTGT 567
QY 368 GAAGAAATATGAACAGGATTCATACAGACCCCTGTGTTCTCAGCCCCAAGAGATCGCGT 427
Db 568 GAAAAAACAGAAATCTGTGTGTGACTGATCCGACAGACTGTTCTGCCAACACAGACGCT 627
QY 428 GCGGATGTTTTTGAGGCCAAGGCCCGGCATGTTTCTCGCGTATCCCAATCACAGACAC 487
Db 628 GCGGGAAGTGAAGAAGTACCGCAGCGTAAACGTTTGGCGGCTATCCGCTGCTTACCGA 687
QY 488 AGGCCGATGGGAGCCGCTTGGTGGCATCATCTCTCCAGGACATTTGATTTTCTCAA 547
Db 688 A-----GAAACGAACTGGTGGGTATTATCACCCGGTCGACGTGCGTTTGTTCAC 738

QY 548 AGAGAGAGACATGACTGTTCTTGGAGAGATATGACAAGAGGAGAGACTTGTTGGT 607
Db 739 CGACCTGAACCAAGCCGGTTAGCGTTTACATGACGCCGAAGAGCCGTCTGTACCCGTGCG 798
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Db 799 TGAAGCTGAAGCCCGTGAAGTGTGCTGGCAAA-----AATGCACGAAGAACCGCTTGA 852
QY 668 AAAGTTGCCCATTTGTAATATGAGATGATGAGCTTGTGGCCATCATTTGCCGACAGACCT 727
Db 853 AAAAGCGCTGGTGGTGTGATGACGAATTCACCTGATCGGCATGATCAGCTGAAGACTT 912
QY 728 GAAGAGAATCGGACTACCCACTAGCCTCCAAAGATGCCAAGAAACACTGCTGTGTGG 787
Db 913 CCAGAAAGCGGAAGCTAAACCGAACCCCTGTAAAGACGACGAAGGCCGCTGCGTGTGG 972
QY 788 GGCAGCCATTGGCAGCTCATGAGGATGACAAGTATAGGCTGAGCTTGCTGGCCAGGCTGG 847
Db 973 TGCAGCGGTTGGCGCAGGTGGGGTTAACGAAGAGCGTGTGACGCGCTGTTGCCGAGG 1032
QY 848 TGTGATGTAGTGGTTTGGACTCTTCCAGGAGAAATTCATCTTCCAATCATATGAT 907
Db 1033 CGTTGACGTTCTGCTGATGCACTCTCCACGCGTCACTGAGAAAGGTGTCTGCAACGTAT 1092
QY 908 CAAGTACATCAAAAGACAATACCCTAATCTCCAAGTCAATTGAGGCAAGTGGTCACTGC 967
Db 1093 CCGTGAAAACCCGTGCTAAATATCCGGATCTGCAAAATTAATCGCGGCAAGTGCAACAGC 1152
QY 968 TGGCCAGGCCCAAGAACCTCATTTGATGACAGGTGTGAGTGGCCCTGCGGGTGGCATGGAG 1027
Db 1153 TGCAGGTGCACGCGCTCTGGCAGAAAGCTGGTTGAGTGGCGTTAAAGTGGCATTTGGCCC 1212
QY 1028 TGGCTCCATCTGCATTAATTCAGGAAGTGTGCTGGCCTGTGGCGGCCCAAGCAACAGCAT 1087
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Db 1453 TTACAAATCTTACCGTGGTATGGGTTCCCTGGCGCGATGTCCAAAGGTTCCCTGACCG 1512
QY 1328 GAACAGATATTTCAAGTGAAGCTGACAAATCAAAAGTGGGCCAGGAGATCTCTGTGCTGT 1387
Db 1513 TTATTTCCAGAGCGATTAACGCTGCCGACAAACTGGTGGCGGAAGCTATGAAGGTGCGGT 1572
QY 1388 GCAGGACAAGGGTCAATCCACAATTTTGTCCCTTAACCTGATTGCTGCTATCC 1440
Db 1573 AGCCTATAAAGTGCCTGAAGAAGATCATTCACACGACAGATGGCGGCTCTGC 1625

RESULT 11

US-09-134-001C-2187
; Sequence 2187, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucelte-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2187
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2187
Query Match 10.8%; Score 179.4; DB 4; Length 1485;
Best Local Similarity 47.5%; Pred. No. 2.1e-45;
Matches 642; Conservative 0; Mismatches 696; Indels 15; Gaps 3;

QY 136 TCACCTACAATGACTTTCTCATTTCTCCCTGGGTACATGCACTTCACTGCAGACCAAGTGG 195
Db 50 TAACATTCGACGACGTGTACATCAATTCAGCTGCATCAGATGTTTACCAAGCGATGTG 109
QY 196 ACCGTACTTCTGCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTTCTCTCCCA 255
Db 110 ACTTAAGTGTCAAAATTAATGAGTAAGATCAAGTTAAACATTCCTGTTATCTCAGAGGTA 169
QY 256 TGGACACAGTCAACAGAGCGTGGGATGGCCATAGCAATGGCGCTTACAGCGGATTTGGCT 315
Db 170 TGGATACAGTAAGTCAATCAAAATGCGCAATTGCTATGGCTGACAAGCGGCTTAAGGTG 229
QY 316 TCATCCACCACACTGTACACCTGAATTTCCAGGCCAATGAAGTTGGAAGTGAAGAAAT 375
Db 230 TTATTCATAGAATATAGGCGGTGGAAGACAAGCAAGCTGATCAGGTACAAAGTTAAACGTT 289
QY 376 ATGACAGGGAATTCATCACAAGACCCCTGTGCTCTCAGCCCAAGATCGCTGCGGATG 435
Db 290 CAGAAATATGTTATTTCTTAACCCGTTCTTCTTAACACCGGAAGAGTGTGTAAGG 349
QY 436 TTTTGAAGGCCAAGGCCCGGATGTTTCTGCGGTATCCCAATCACAAGACACAGCGCGGA 495
Db 350 CTGAAGCATTAATGATGAATTAACCGTATCTCTGTTACCCATTTGTCGATAA--TCAAG 406
QY 496 TGGGAGCCGCTTGGTGGGATCATCTCTCCAGGACATTTGATTTTCTCAAGAAGAGG 555
Db 407 AGGATCGCAAGTTGATGGATTTTAAACAATCGTGAATTTACGTTTATTTGAAGATTTT 466
QY 556 AACATGACTGTTTCTTGAAGAGATAATGACAAGAGGAAAGACTTGGTGTAGCCCCC 615
Db 467 CAATTAATAATATCAGATGTATGAC-----GAAGATAATTTAATAACAGCTCCAG 517
QY 616 GCAGCATCACACTGAAGAGCAAAATGAATTTCTGCAGCCGACGACAAGAGGAAAGTTGC 675
Db 518 TTGGTACGACTTTAGATGAAGCCGAGGCTATTCTTCAAAAACATAAGATTGAGAAACTTC 577
QY 676 CCATTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGACCTGGAACAAGA 735
Db 578 CATTAGTA--GAAATGTCGTTTGAAGAGATTAACTACTATTAAAGATATTGAATAAAG 634
QY 736 ATCGGAGACTACCCACTAGCCTCCCAAGATGCCAAGAAACAGCTGCTGTGGGCAAGCA 795
Db 635 TACTTGAATTTCCATATGACGCTAAAGATGAACATGGCAGATTGTTAGCTGCGGCAAGCA 694
QY 796 TTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGTCTGCCAGGCTGGTGTGATG 855
Db 695 TCGGTACGCTTAAGATTAAGTAATTCGTGCACAAAACACTAGTTGAAGCTGGCGGTAGATG 754
QY 856 TAGTGGTTTGGACCTTTCACAGGGAATTTCCATCTTCCAGATCAATATGATCAAGTACA 915
Db 755 CATTAATTAATGATACAGCTCATGCTCATTTCTTAAGCGGTTATTATTAACAGTTAAACACA 814
QY 916 TCAAGACAATATACCCTAATCTCCAAGTCAATTTGGAGCCAATGTGTCACCTGCTGCCAGG 975
Db 815 TCAAGGAACATATCTCGAAATTTACTGTGTGCTGCTGTAACGTAGCGACTGCAAGCAAGCA 874
QY 976 CCAAGAACCTCATTTGATGCAAGGTGTGATGCCCTGCGGCTGGGCATGGGAAGTGGCTCCA 1035
Db 875 CACGTGCTTATTTGAAGCGGGTGGCGATGTTGTTAAAGTAGGATTTGGTCCAGGCTCAAA 934

QY	1036	TCTGCATTATCCAGGAAGTGCCTGGCCCTGTGGCGCGGCCCAAGCAACAGCAGTGTACAAAG	1095
Db	935	TTTGACACAACACGTTGTTCTTGCAGGTGTAGGTGTGCCTCAAAATTACAGCAGTTATATGATT	994
QY	1096	TGTATGAGTATGCACGCGCCTTTGGTGTCCGGTCATTGCTGATGGAGGAATCCAAATG	1155
Db	995	GTGCTACAGAAGCCCGTAAGCATGGTAAGGCTATTATTGCTGATGGTGTATTAACTTCT	1054
QY	1156	TGGTCATATTGGGAAAGCCTTGGCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCC	1215
Db	1055	CAGTGATATTATCAAAAGCATTAGCTGCTGGTGTGTCATGCGGTTATGTTAGGTAGTTGT	1114
QY	1216	TGGCTGCCACCACCTGAGGCCCTGTGTAATACTTCTTTTCCGATGGGATCCGGCTAAAGA	1275
Db	1115	TAGCTGTACAGAGAAGATCCTGGTGCACTGAAGTATTTCCAAGGTAGACAATATAAAG	1174
QY	1276	AATATCGCGGTATGGGTCTCTCGATGCCATGGACAAGCACCTCAGCAGCCAGAACAGAT	1335
Db	1175	TTTATCGCGGCATGGGATCTTTAGGTGCTATGGAAAAAGTTCAATGATCGTTACTTCC	1234
QY	1336	ATTTCAGTGAAGCTGACAAAATCAAAAGTGGCCAGGAGTGTCTGGTCTGTGCAGACA	1395
Db	1235	AAGAAGATAAAACACACCAGAAAATTTGTTCTCGTAAGGTATTGAAGGTCGTACAGCTTATA	1294
QY	1396	AAGGTCATCCACAAATTTGTCCCTTACCCTGATTGCTGGCATCCAACACTCATGCGCAGG	1455
Db	1295	AAGGACCATTTACAAAGATACAAATTTATCAACTTATGGGTGGCGTTAGAGCTGGCATGGGTT	1354
QY	1456	ACATTGGTGGCAAGAGCTTGACCCCAAGTCCGAG	1488
Db	1355	ATACTGGTTCAGAAAAACCTTAAAAAAATTACGTG	1387

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RESULT 12
US-09-221-017B-497
; Sequence 497, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: ROSS, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Montroy, Gladys H
; REGISTRATION NUMBER: 32,430

```

```

? REFERENCE/DOCKET NUMBER: 27340-20021.00
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-813-5600
? TELEFAX: 650-494-0792
? TELEX: 706141
? INFORMATION FOR SEQ ID NO: 497:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5884 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: UNKNOWN
? ORIGINAL SOURCE:
? ORGANISM: PORYPHYROMONAS GINGIVALIS
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 1...5884

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[illegible]

[illegible]

Db	119	GTAAAAATTGCCGAGATTGCTGCATTTTCCAGATCGCACTTTGATTTGCTGGAAATATTG	178
QY	961	TCACGTGCTGCCAGGCCAAGAACCTCATTTGATGACAGTGGATGCCCTGCGGGTGGCA	1020
Db	179	CTACTGCTGAAGGTGCACGTGCCCTTTATGAAGCGGGCTAGACGTTGTTAAGTTGCTA	238
QY	1021	TGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCCCTGTGGGGGCCCAAGCA	1080
Db	239	TTGGACCAGGTTCTATCTGTACTACTCGTGTGATTTGCTGTGTTGGTGTTCGCCAAGTAA	298
QY	1081	CAGCAGTGTACAAAGGTGTATGAGTATGCACGGCCGCTTTGGTGTCCGGTCAATGCTGATG	1140
Db	299	CAGCTATCTACGATGCTGCAGCTGTTGGCGCGCAATATGTAAACGATTATTTGCTGACG	358
QY	1141	GAGGAATCCAAAATGTGGCTATATTGCGAAAGCCTTGGGCCCTCCACAGTCA	1200
Db	359	GTGGGATCAAGTATTCTGAGAGATTGTTAAAAGCACTTGCTGCAGGTGGAAAATGCTGTTA	418
QY	1201	TGATGGCTCTCTCCTGCTGCCACCACCTGAGGCCCTGTGTGATACTCTCTTTCCGATG	1260

```

RESULT 13
US-08-961-527-329
: Sequence 329, Application US/08961527
: Patent No. 6420135
:
: GENERAL INFORMATION:
: APPLICANT: Charles Kunsch
: TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
: NUMBER OF SEQUENCES: 391
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/961,527
:
: FILING DATE:
:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
:
: FILING DATE:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Brookes, A. Anders
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB340P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 329:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1653 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
US-08-961-527-329

```

QY 1261 GGATCCGGCTAAGAATATCGCGGTATGGGTTCTTCGATGCCATGGACAA 1312
1 1111 1111111111 11 1111111111
Db 479 GACGTAATTCAGACTTACCGTGTATGGATCAATTGCTGCTATGAAGAA 530

RESULT 14
US-08-774-169-2
; Sequence 2, Application US/08774169
; Patent No. 5756332
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL GUANOSINE MONOPHOSPHATE REDUCTASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,169
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0182 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEEX:

	Query Match	7.28;	Score 118.4;	DB 4;	Length 1653;
	Best Local Similarity	53.28;	Pred. No. 1.8e-26;		
	Matches 251;	Conservative	0;	Mismatches 221;	Indels 0;
					Gaps 0;
QY	841 AGCGTGTGTGGATGAGTGGCTTTTGGACTCTTCCAGGGAATTCCA				CTTCAGATCA 900
DB	59 AGGCAGAGCGGATGCGATTGTTATTGACTGCACATGTCATTTCTG				CAGTGTCTTGC 118
QY	901 ATATGATCAAGTACATCAAGACAATATACCCTAATCTCCAGTCATTGG				AAGCAATGTGG 960

```

; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1843 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; IMMEDIATE SOURCE:
;
; LIBRARY: Consensus
;
; CLONE: Consensus
;
US-08-774-169-2

```

```

Query Match      4.98; Score 81.6; DB 1; Length 1843;
Best Local Similarity 46.9%; Pred. No. 5e-15;
Matches 255; Conservative 0; Mismatches 289; Indels 0; Gaps 0;

QY   772 AACAGCTGCTGTGTGGGCACGCCATTGGCAGTATGAGATGACAAGTAGATAAGCGTGACT 831
       ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    625 AGCATCTGGCTGCCAGCTCAAGCCACAGGCTCTTCGACTTTGAGCAGCTGGAACAGATCC 684
QY     832 TGCTCGCCCAGCGCTGGTGTGATGTAGTGGTTTTGGACTCTTCCAGGAAATTCATCT 891
       || || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    685 TGAAGCTATTCCCCAGGTGAAGTATATATGCCCTGGATGTGGCAAATGGCTACTGTAAC 744
QY     892 TCAGATCAATATGATCAAGTACATCAAGAACAATACCCTAATCTCCAAGTCAATTGGAG 951
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    745 ACTTTGTGAATTTGTAAAAAGATGTACGGAAGCGCTTCCCCAGCACACCATCATGGCAG 804
QY     952 GCAATGTGTGCTACTGCTGCCAGGCCAAGAACCCTCATTTGATGACGTTGGATGCCCTGC 1011
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    805 GGAATGTGTACAGAGAGATGTTAGAGAAGATCATCTCTTTGGGGCTGACATCATCA 864
QY    1012 GGGTGGCATGGGAAGTGGCTCCATCTGCATTATCCAGAACTGTGCTGTGGCGGCC 1071
        ||||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    865 AAGTGGGAATTTGGCCAGGCTCTGTGTACTACTCGGAACAANAAGTGGAGTGGGTATC 924
QY    1072 CCCAAGCAACAGCAGTGTACAAAGGTGTAGATGACATGACACGGCGCTTTGGTTCGGGTCA 1131
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    925 CACAGCTCAGCGCAGTGATGGAGTGTGACAGATGCTGCTCATGGCCTCAANGGCCACATCA 984
QY    1132 TTGCTGATGAGAAATCCAAAATGTGGGTCTATTTGCGAAAGCCTTGGCCTTGGGGCCT 1191
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    985 TTTCAGATGAGGTTGCAGCTGTCTGCGGATGTGGCCAAGGCTTTTGGGCAGAGACTG 1044
QY    1192 CCACAGTCATGATGGGCTCTCTCCTGGCTGCCACCACCTAGAGGCCCTGGTAATACTTCT 1251
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1045 ACTTCGTGATGCTGGGTGGCATGTCTGGCTGGGCACAGTAGATCAGGTGGTGAGCTCATCG 1104
QY    1252 TTTCGATGGGATCCGGCTTAAGAATATCGCGGTATGGTCTCTCGATGCCATGGACA 1311
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1105 AGAGGGATGGCAAGATACAAAGCTCTTCTATGGAATGAGTTCTGAATGGCCATGAAGA 1164

QY    1312 AGCA 1315
        || |
Db    1165 AGTA 1168

RESULT 15
US-08-961-527-126/c
: Sequence 126, Application US/08961527
: Patent No. 6420135
: GENERAL INFORMATION:
: APPLICANT: Charles Kunsch
: TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
: NUMBER OF SEQUENCES: 391
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/961,527
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;

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Query Match	4.6%	Score 75.8	DB 4	Length 13121
Best Local Similarity	47.7%	Pred. No. 1.1e-12		
Matches 255	Conservative 0	Mismatches 277	Indels 3	Gaps 1
QY 767	CAAGAAACAGCTGCTGTGTGGGCGACCATTTGGCACTCATGAGAGTGAACAAGTATAGGCT	826		
Db 12794	CAATCAAGGGCTCATTTGCTTCTATCTGTGCGGTGTTAAGAAATATGAGTATGATTTTGT	12735		
QY 827	GGACTTGTCTGCCAGGCTGGTGTGATGTAGTGTGTTTGACTCTTCCAGGAAATTC	886		
Db 12734	TAGCCAGCTCAAGGCTGATTACTCCTGACGATATATCACTATTGATTTGCTCATGGTCATGC	12675		
QY 887	CATCTTCCAGATCATATATGATCAAGTACATCAAGAACAATACCCTTATCTCCAAGTCAT	946		
Db 12674	GGATAGCGTGATTTCTATGATTCACACATCAAGAAGAATTGCCAGATACCTTTGTGTCAT	12615		
QY 947	TGAGGCAATGTGTGTCACGTGCTGCCAGGCCAAGAACCTCATTTGATGACGCTGTGATGC	1006		
Db 12614	TGCTGGAATGTGGGAACACAGAAAGCTGTGCGTGAATTGAAAATGCTGCTGCGGATGC	12555		
QY 1007	CCTGGGGTGGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGCGCTGTGG	1066		
Db 12554	TACTAAGTCCGAATCGGTCTCGTAAAGTTTGTATCACCAGAAGTTAAGACTGCTTTTGG	12495		
QY 1067	GCGGCCCCAAGCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCGCTTGTGTTCC	1126		
Db 12494	TA--CAGGTGGTTGGCAGTTGGCTGCTCTTACCCCTGGTGTGCCAAGGCTGCGCGTAACC	12438		
QY 1127	GGTCATTTGCTGATGAGGAATCCAAAAATGTGGTCATATTGCGAAAGCCTTGGCCCTTGG	1186		
Db 12437	GATTATCGCTGATGAGGAATTCGTACTACAGGTGATTTGCTAAAGTCTATCCGCTTCGG	12378		
QY 1187	GGCCTCCACAGTCATGATGGGCTCTCTCTGCTGCGCCACCACTGAGGCCCTGTGTAATA	1246		
Db 12377	TGCTAGCATGATCATGATTTGTTCCCTCTTTGACGACACACATTTGAAGTCCAGGAAAC	12318		
QY 1247	CTTCTTTTCCGATGGGATCCGGCTAAAGAATATCCGGGTATGGGTTCTCTCGAT	1301		
Db 12317	GATTGAAGTGCATGTGTAACACAGTTCAAAGAATATTTATGTTACGCTCACAAATAT	12263		

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Search completed: February 12, 2003, 20:32:40
Job time : 101 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 15:56:59 ; Search time 1251 Seconds
(without alignments)
11900.193 Million cell updates/sec

Title: US-09-846-637C-3
Perfect score: 1654
Sequence: 1 gaattcgagcggtcctcgcga.....gtttagaaagcccgaattc 1654

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32 08132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrl: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1601	96.8	1691	11	BC009236	BC009236 Homo sapi
2	1305.4	78.9	1655	11	AK002676	AK002676 Mus muscu
3	1252.6	75.7	1650	11	AK011777	AK011777 Mus muscu
4	1043.4	63.1	1075	9	AL565764	AL565764 AL565764
5	1028.8	62.2	1065	9	AL535072	AL535072 AL535072
6	1017.6	61.5	1049	9	AL539530	AL539530 AL539530

7	987	59.7	1011	9	AL551909	AL551909 AL551909
8	973.4	58.9	1028	9	AL514250	AL514250 AL514250
9	959.4	58.0	994	9	AL560269	AL560269 AL560269
10	925.8	56.0	996	9	AL516817	AL516817 AL516817
11	922.8	55.8	1061	13	BM550826	BM550826 AGENCOURT
12	920.8	55.7	968	9	AL542763	AL542763 AL542763
13	917.4	55.5	953	9	AL534371	AL534371 AL534371
14	911	55.1	1020	14	B0278808	B0278808 AGENCOURT
15	910	55.0	1023	14	B0058198	B0058198 AGENCOURT
16	907.8	54.9	987	14	B0958566	B0958566 AGENCOURT
17	907	54.8	923	9	AL539870	AL539870 AL539870
18	903.6	54.6	1028	13	BM558422	BM558422 AGENCOURT
19	899.2	54.4	1067	13	BM560358	BM560358 AGENCOURT
20	897	54.2	1049	13	BM551559	BM551559 AGENCOURT
21	896.8	54.2	1017	14	B0063190	B0063190 AGENCOURT
22	894.2	54.1	957	9	AL575480	AL575480 AL575480
23	893.6	54.0	1002	9	AL539529	AL539529 AL539529
24	888.2	53.7	1102	13	BM464439	BM464439 AGENCOURT
25	888	53.7	1033	14	B0064687	B0064687 AGENCOURT
26	887	53.6	988	14	B0066491	B0066491 AGENCOURT
27	886	53.6	1060	14	BM927366	BM927366 AGENCOURT
28	884.8	53.5	902	9	AL557223	AL557223 AL557223
29	881.6	53.3	1055	14	BM927655	BM927655 AGENCOURT
30	880.8	53.3	1105	14	BM799870	BM799870 AGENCOURT
31	879.4	53.2	1015	14	B0065663	B0065663 AGENCOURT
32	879.2	53.2	1018	9	AL581748	AL581748 AL581748
33	873.4	52.8	889	9	AL547478	AL547478 AL547478
34	873.4	52.8	926	9	AL577863	AL577863 AL577863
35	873	52.8	1144	14	BM810254	BM810254 AGENCOURT
36	871.4	52.7	1012	9	AL517322	AL517322 AL517322
37	871.4	52.7	1061	13	BM477104	BM477104 AGENCOURT
38	870.8	52.6	947	14	B0918379	B0918379 AGENCOURT
39	870.6	52.6	897	14	B0927530	B0927530 AGENCOURT
40	868.2	52.5	1030	14	BM810336	BM810336 AGENCOURT
41	868	52.5	945	14	B0941627	B0941627 AGENCOURT
42	867.6	52.5	1050	14	BM909098	BM909098 AGENCOURT
43	867.4	52.4	966	14	B0930524	B0930524 AGENCOURT
44	867	52.4	920	9	AL567179	AL567179 AL567179
45	866.2	52.4	936	14	B0927109	B0927109 AGENCOURT

ALIGNMENTS

RESULT 1	BC009236	1691 bp	mRNA	linear	HTC 12-JUL-2001
LOCUS	Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone IMAGE:2988188, mRNA.				
DEFINITION	Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone IMAGE:2988188, mRNA.				
ACCESSION	BC009236				
VERSION	BC009236.1	GI:14714378			
KEYWORDS	HTC.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1 (bases 1 to 1691)				
TITLE	Strausberg, R.				
JOURNAL	Direct Submission				
REMARK	Submitted (06-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
COMMENT	NIH-MGC Project URL: http://mgc.ncl.nih.gov Contact: MGC help desk				

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadane@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia

Greene, Mark Ketteman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 3 Row: 5 Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 1702963
This clone has the following problem: frame shifted.

FEATURES
Source
1. 1691
/organism="Homo sapiens"
/db_xref="LocusID:3615"
/db_xref="IMAGE:2988188"
/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_15"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

BASE COUNT 467 a 411 c 448 g 365 t
ORIGIN

Query Match 96.8%; Score 1601; DB 11; Length 1691;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1618; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 17 CGGAGACACGGCGGTGTCCTGTGTTGGCCATGGCCGACTACCTGATTAGTGGGGCAC 76
Db 10 CGGAGACACGGCGGTGTCCTGTGTTGGCCATGGCCGACTACCTGATTAGTGGGGCAC 69
QY 77 GTCTACGTCGACAGACGAGCTACACAGCAGCAGCAGCTCTTCAACTGCGGAGACGGCCT 136
Db 70 GTCTACGTCGACAGACGAGCTACACAGCAGCAGCAGCTCTTCAACTGCGGAGACGGCCT 129
QY 137 CACCTACATGACTTTCTCATTTCTCCCTGGGTACATGACTTCATCTGCAGACCAGGTGGA 196
Db 130 CACCTACATGACTTTCTCATTTCTCCCTGGGTACATGACTTCATCTGCAGACCAGGTGGA 189
QY 197 CCTGACTTCTGCTGTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCAT 256
Db 190 CCTGACTTCTGCTGTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCAT 249
QY 257 GGACACAGTCACAGAGGCTGGGATAGCAGATGGCGCTTACAGGCGGTATTGGCTT 316
Db 250 GGACACAGTCACAGAGGCTGGGATAGCAGATGGCGCTTACAGGCGGTATTGGCTT 309
QY 317 CATCCACCACAACCTGTACACCTGTAATTCAGGCGCAATGAAGTTCGAAAGTGAAGAATA 376
Db 310 CATCCACCACAACCTGTACACCTGTAATTCAGGCGCAATGAAGTTCGAAAGTGAAGAATA 369
QY 377 TGAACAGGGAATTCATCACAGACCCCTGTGCTCTCAGCCCCCAAGATCGCGTGGGATGT 436
Db 370 TGAACAGGGAATTCATCACAGACCCCTGTGCTCTCAGCCCCCAAGATCGCGTGGGATGT 429
QY 437 TTTTGAGGCCCAAGGCCCGCATGTTTCTGCGGTATCCCAATCACAGACAGAGCGCGAT 496
Db 430 TTTTGAGGCCCAAGGCCCGCATGTTTCTGCGGTATCCCAATCACAGACAGAGCGCGAT 489
QY 497 GGGAGCCGCTTGTGGCATCATCTCTCCAGGAGACATTGATTTTCTCAAGAGAGAGA 556
Db 490 GGGAGCCGCTTGTGGCATCATCTCTCCAGGAGACATTGATTTTCTCAAGAGAGAGA 549
QY 557 ACATGACTGTTTCTTGGAAGAGATTAAGCAAAAGAGGAGACTTGGTGGTAGCCCCCG 616
Db 550 ACATGACTGTTTCTTGGAAGAGATTAAGCAAAAGAGGAGACTTGGTGGTAGCCCCCG 609
QY 617 CAGATCACACTGAAGGAGGCAAAATGAATTTCTGCAGCGCAGACAGAAAGGAAAGTTGCC 676
Db 610 AGGCAATCACACTGAAGGAGGCAAAATGAATTTCTGCAGCGCAGACAGAAAGGAAAGTTGCC 669
QY 677 CATTTAAATGAAGATGATGAGCTGTGCCATCATTTGCCCGGACAGACCTGAAGAAGAA 736
Db 670 CATTTAAATGAAGATGATGAGCTGTGCCATCATTTGCCCGGACAGACCTGAAGAAGAA 729

QY 737 TCGGACTACCCACTAGCCTCCAAAGATGCCCAAGAAACAGCTGCTGTGCGGCAGCCAT 796
Db 730 TCGGACTACCCACTAGCCTCCAAAGATGCCCAAGAAACAGCTGCTGTGCGGCAGCCAT 789
QY 797 TGGCACTCATGAGGATGACAAATATAGGCTGACTTGTCCGCCAGGCTGTGTGATGT 856
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QY 857 AGTGTTTTGACTCTTCCAGGAAATTCATCTTCCAGATCAATATGATCAAGTACAT 916
Db 850 AGTGTTTTGACTCTTCCAGGAAATTCATCTTCCAGATCAATATGATCAAGTACAT 909
QY 917 CAAAGCAAAATACCCTAATCTCCAAGTCATTGGAGCAATGTGTCACTGTGCCAAGC 976
Db 910 CAAAGCAAAATACCCTAATCTCCAAGTCATTGGAGCAATGTGTCACTGTGCCAAGC 969
QY 977 CAAGAACCTCATTTGATGCAGGTGTGATGCCCTGCCGGTGGCATGGGAAGTGGCTCAT 1036
Db 970 CAAGAACCTCATTTGATGCAGGTGTGATGCCCTGCCGGTGGCATGGGAAGTGGCTCAT 1029
QY 1037 CTGCATTTACAGGAAGTGTGCTGGCCTGTGGCGGCCCAAGCAACAGAGTGTACAGGT 1096
Db 1030 CTGCATTTACAGGAAGTGTGCTGGCCTGTGGCGGCCCAAGCAACAGAGTGTACAGGT 1089
QY 1097 GTATGATATGCACGCGCTTGTGTCTCCGGTCATTTGATGAGGAATCCAAATGT 1156
Db 1090 GTATGATATGCACGCGCTTGTGTCTCCGGTCATTTGATGAGGAATCCAAATGT 1148
QY 1157 GGTCTATTTGCGAAAGCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCT 1216
Db 1149 GGTCTATTTGCGAAAGCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCT 1208
QY 1217 GGCTGCCACCACTGAGGCCCCGTGTAATCTCTTTCCGATGGGATCCGGCTAAAGAA 1276
Db 1209 GGCTGCCACCACTGAGGCCCCGTGTAATCTCTTTCCGATGGGATCCGGCTAAAGAA 1268
QY 1277 ATATCGCGTATGGGTCTCTCGATGCCATGGACAAAGCACCCTCAGCAGCAAGACAGATA 1336
Db 1269 ATATCGCGTATGGGTCTCTCGATGCCATGGACAAAGCACCCTCAGCAGCAAGACAGATA 1328
QY 1337 TTTCAGTGAAGCTGACAAATCAAAAGTGCCCCAGGAGTGTCTGTGTCAGAGCAA 1396
Db 1329 TTTCAGTGAAGCTGACAAATCAAAAGTGCCCCAGGAGTGTCTGTGTCAGAGCAA 1388
QY 1397 AGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGCATCCAAACATCATGCCAGA 1456
Db 1389 AGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGCATCCAAACATCATGCCAGA 1448
QY 1457 CATTTGCCAAGAGCTTGACCCAGTCCAGGCCATGATGATCTGGGGAGCTTAAGTT 1516
Db 1449 CATTTGCCAAGAGCTTGACCCAGTCCAGGCCATGATGATCTGGGGAGCTTAAGTT 1508
QY 1517 TGAGAGAGAACGTCTCAGCCCAAGTGAAGGTGGCGTCCATAGCCTCCATTCGTATGA 1576
Db 1509 TGAGAGAGAACGTCTCAGCCCAAGTGAAGGTGGCGTCCATAGCCTCCATTCGTATGA 1568
QY 1577 GAAGCGGCTTTCTGAAGAAAGGATCCAGCACACCTCTCGGTTTTTTTCAATAAAGT 1636
Db 1569 GAAGCGGCTTTCTGAAGAAAGGATCCAGCACACCTCTCGGTTTTTTTCAATAAAGT 1628
QY 1637 TTAGAAAGA 1645
Db 1629 TTAGAAAGA 1637

RESULT 2 1655 bp mRNA linear HTC 19-JAN-2002
AK002676
LOCUS AK002676
DEFINITION Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610025012:inosine 5'-phosphate dehydrogenase 2, full insert sequence.
ACCESSION AK002676
VERSION AK002676.1 GI:12832835

Db 86 GCGAGGACCTCTTACGTGCGGACGACGGGCTCACAGCGCA -CAGCTCTTCAACTGCG 144

QY 127 GAGACGGCCTCACCTACAATGACTTCTTCATTTCTCCCTGGGTACATCGACTTCACCTGCAG 186

Db 145 GGGACGGCCTCACCTACAATGATTTTCTCATTTCTCCTGGGTATATCGACTTCACCTGCAG 204

QY 187 ACCAGGTGGACCTGACTTCTGCTCTGACCAAGAATAATCATTCTTAAGACCCCACTGGTTT 246

Db 205 ATCAGGTGGACTTGACGCTGCTCTAATAAGAGATTACACTAAGACCCCATTTGGTTT 264

QY 247 CCTCTCCCATGGACACAGTCACAGAGGCTGGGATGGCCATAGCAATGGCGTTACAGCG 306

Db 265 CCTCACCATGGACACTGTCCAGAGGCTGGAATGGCCATGGCGTTACAGGAG 324

QY 307 GTATTGGCTTCATCCACCACACACTGTACACCTGAATTCCAGGCCAATGAAGTTGGAAG 366

Db 325 GTATTGGTTTCATCCACACACTGCACACCTGAATTCAGGCCAATGAAGTTGGAAG 384

QY 367 TGAAGAAATATGAACAGGAGGATTCATCACAGACCCCTGTGCTCAGCCCCAAGATCGCG 426

Db 385 TGAAGAAATACGAACAGGAGATTCACTGACCCCGTGGTCTTAGCCCCAAGATCGTG 444

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Db 445 TACGCGATGTTTTTGAGGCCAAGCCAGGCATGGCTTCTGTGTATCCCATCACAGATA 504

QY 487 CAGGCGGATGGGAGCGCGTGTGGGCATCATCTCCTCCAGGACATTGATTTTCTCA 546

Db 505 CAGGCGGATGGGAGTGCATTGTGGGCATCATCTCCTCAAGGGACATTGATTTCTCTCA 564

QY 547 AAGAGGAGAACATGACTGTTTCTTGGAAGAGATATGACAAAGAGGGAGACTTGCTG 606

Db 565 AGAGGAGAGACATGACCGGTTCTTGGAAGAGATCATGACTTAAGAGGGAGATTGCTG 624

QY 607 TAGCCCCCGCAGCATCACACTGAGGAGGCAAAATGAATTCGACGCGCAGCAAGAAG 666

Db 625 TCGCCCTGCGCGCGTCACTCTGAAGAGGCAAAATGAGATTCTGCAGCAAGTAAAAAG 684

QY 667 GAAAGTTGCCATTGTAAATGAAGATGATGAGCTTGTGGCCATCATTGCCCGACAGACC 726

Db 685 GAAAGTTGCCATTGTGAATGAATGATGAGCTGTAGCCATCATTTGCCCGACAGACC 744

QY 727 TGAAGAGAATCGGACTACCCACTAGCCTCCAAAGATGCCAAGAAACAGCTGCTGTG 786

Db 745 TAAAGAGAATCGTGATTACCCCGCGCTCCAAAGATGCCAAGAACTACTGCTGTG 804

QY 787 GGGACCCATTGGCACTCATGAGATGACAAGTATAGGCTGACTTGCCTCGCCAGCGTG 846

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Db 865 GTGTGATGTAGTGGTTTGGACTCTTCCAGGGAATTCATCTTCCAAATCAATATGA 924

QY 907 TCAAGTACATCAAAAGACAATAATACCCTAATCTCCAAGTCAATTGAGGCAATGTGTCAC 966

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QY 967 CTGCCCAGGCCAAGAACCTCATTTGATGCAAGGTGTGATGCCCTGCGGGTGGGCATGGAA 1026

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QY 1147 TCCAAATGTGGGTCAATTGTGCAAGCCTTGCGCCTTGGGGCTCCACAGTCATGATGG 1206

Db 1165 TCCAAATGTGGTCATATTGCCAAAGCTTTGGCTCTTGGGGCTTCCACAGTCATGATGG 1224

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Db 1225 GCTCCCTCCTGGCTGCCACCACCTGAGGCCCTTGGCGAGTACTTCTTCTCAGATGGGATCC 1284

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Db 1285 GGCCTAAGAAATACCAGAGTATGGGTTCTCTTGATGCCATGACAACATCTCAGCAGCC 1344

QY 1327 AGAAGATATTTTCAAGTGAAGCTGACAAATCAAAAGTGGCCCCAGGAGTGTCTGCTG 1386

Db 1345 AGAACCGATACTTCAAGTGAAGCTGACAAATCAAAAGTGGCCCCAAGGAGTTTCAGGGCAG 1404

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QY 1447 CATGCCAGACATTGTTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTGTGGG 1506

Db 1465 CCTGTACAGACATTGTTGCCAAGAGTTTAACCCAAGTCAGAGCCATGATGTACTCGGGG 1524

QY 1507 AGCTTAAGTTTGAGAAGAGACGTCCTCAGCCCAAGTGAAGGTGGCTCCATAGCCTCC 1566

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Db 1585 ATTCGTACGAGAAACGCTTTTCTGAAAAACAGATCCAGTATATGCTTGAATTTTCAAT 1644

QY 1627 CAA 1629

Db 1645 AAA 1647

RESULT 3
AK011777
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1650 bp mRNA linear HTC 19-JAN-2002
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:261004P12:inosine 5'-phosphate
dehydrogenase 2, full insert sequence.
AK011777
AK011777.1 GI:12848115
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:261004P12.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
MEDLINE
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
2049374
MEDLINE
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format

Db	803	GGGC--GCCATTGCAC	TGAGGATGACAA	GTATAGGCTTGAC	TTACTGGCCCTTGCTG	860
QY	847	GTGTGGATGTAGTGT	TTTGACTCTTCC	CAGGAAATTCAT	CTTCCAGATCAATATGA	906
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QY	907	TCAAGTACATCAAA	GACAAATACCTA	TCTCCAAGTCAT	TGGAGGCAATGTGTCATG	966
Db	921	TCAATATACATCA	AGGAGATATCC	AGCTCTACAGTC	ATGTGGAAGCAATGTAGTCACTG	980
QY	967	CTGCCAGGCCAAGA	ACCTCATTTGAT	GCAGTGTGAGT	GCCCTGCGGGTGGGATGGGAA	1026
Db	981	-TGGCAAGCCAA	GAACCTCATAG	ATGCAGTGTAG	ATGCTTTGGAGTCGGCATGGGA	1039
QY	1027	GTGGCTCCATCTG	CATTTACAGGA	AGTGTGCTGG	CGCTGTGGGGCCCCCAAGCAACAGCAG	1086
Db	1040	GTGGTTCATCTG	CATCACCAGAA	GTGTGGCGCTG	TGGGGGCCCCCAAGCCACAGCAG	1099
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QY	1207	GCTCTCTCTG	GCTGCACCA	CTGAGGCC	CTGTGTAATCTCTTTCCGATGGATCC	1266
Db	1220	GCTCCTCTCTG	GCTGCACCA	CTGAGGCC	CTGTGTAATCTCTTTCCGATGGATCC	1279
QY	1267	GGCTAAGAAAT	ATATCGCGT	ATGCGTTCT	CTCGATGCGCAAGACACCTCAGCAGCC	1326
Db	1280	GGCTAAGAAAT	ATATCGCGT	ATGCGTTCT	CTCGATGCGCAAGACACCTCAGCAGCC	1339
QY	1327	AGACAGATATT	TTCAGTGAAG	CTGACAAAT	CAAGTGGCCAGGGAGTGTCTGCTGCTG	1386
Db	1340	AGACCCGATAC	TCTCAGTGA	AGCTGACAA	ATCAAAAGTGCCCCAAGAGATTTCAGGGGCAG	1399
QY	1387	TGCAGGACAA	AGGGTCAAT	CCACAAAT	TTTGCTCCCTTACCTGATTTGCTGGCATCCAACACT	1446
Db	1400	TGCAGGACAA	AGGGGTCTAT	CCACAAAT	TTTGCTCCCTTACCTGATTTGCTGGCATCCAACACT	1459
QY	1447	CATGCCAGG	ACATTTGTC	CCCAAGCT	TGACCCCAAGTCGCAGCATGATGTACTCTGGGG	1506
Db	1460	CTGTCAAG	ACATTTGTC	CCCAAGCT	TGACCCCAAGTCATGATGTACTCTGGGGG	1519
QY	1507	AGCTTAAGT	TTGAGAGAG	AAACGTC	TCAGCCAGGTGAAGGTGGCTCCATAGCCTCC	1566
Db	1520	AGCTTAAGT	TTGAGAGAG	AAACGTC	TCAGCCAGGTGAAGGTGGCTCCATAGCCTCC	1579
QY	1567	ATTCTATGA	GAAGCGCT	TTTCTGA	AAAGGATCCAGCACACCTCCTCGGTTTTTTT	1626
Db	1580	ATTCTATGA	GAAGCGCT	TTTCTGA	AAAGGATCCAGCACACCTCCTCGGTTTTTTT	1639
QY	1627	CAA 1629				
Db	1640	AAA 1642				
RESULT 4						
LOCUS	AL565764	1075 bp	mRNA	linear	EST 16-FEB-2001	
DEFINITION	AL565764 LTI_FL013_FBrn1	Homo sapiens	CDNA clone	CS0DF007YL07	3	
ACCESSION	AL565764		prime, mRNA	sequence.		
VERSION	AL565764					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 1075)					
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.					

TITLE	Full-length cDNA libraries and normalization									
JOURNAL	Unpublished (2001)									
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.									
FEATURES	Location/Qualifiers									
source	1. 1075 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DF007YL07" /clone_lib="LTI_FL013_FBrn1" /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)" /lab_host="DH10B" /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"									
BASE COUNT	237	a	303	c	253	g	281	t	1	others
ORIGIN										
Query Match	63.1%; Score 1043.4; DB 9; Length 1075;									
Best Local Similarity	98.6%; Pred. No. 1.2e-297;									
Matches 1062; Conservative	1;	Mismatches	12;	Indels	2;	Gaps	1;			
QY	545	CAAAGAGGAGACATGAC	GTGTTCTTGGAGAGATAATGACAAAGAGGAAAGACTTGGT	604						
Db	1075	CAAAGAGRGGAACATGAC	TGTTCTTGGAAAGATAATGACAAAGAGGAAAGACTTGGT	1016						
QY	605	GGTAGCCCCCGCAGCAT	CACACTGAAGGAGGCAAAATGAATTTCTGCAGCGCAGCAAGAA	664						
Db	1015	GGTAGCCCCCTGCAGGC	ATCACACTGAAGGAGGCAAAATGAATTTCTGCAGCGCAGCAAGAA	956						
QY	665	GGGAAGTTGCCATTTG	TAAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGA	724						
Db	955	GGGAAGTTGCCATTTG	TAAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGA	896						
QY	725	CCTGAAGAAGATCGGG	ACTACCCACTAGCCCTCCAAGATGCCAAGAACAGCTGCTGTG	784						
Db	895	CCTGAAGAAGATCGGG	ACTACCCACTAGCCCTCCAAGATGCCAAGAACAGCTGCTGTG	836						
QY	785	TGGGCGCCCATTTGG	CACTCATGAGATGACAAAGTATAGCTTGACTGCGCCAGGC	844						
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QY	845	TGGTGTGATGTAGT	GTTTGGACTCTTCCAGGAAATTCATCTTCCAGATCAATAT	904						
Db	775	TGGTGTGATGTAGT	GTTTGGACTCTTCCAGGAAATTCATCTTCCAGATCAATAT	716						
QY	905	GATCAAGTACATCA	AGACAAATACCTAATCTCCAAGTCATTTGGAGGCAATGTGTCAC	964						
Db	715	GATCAAGTACATCA	AGACAAATACCTAATCTCCAAGTCATTTGGAGGCAATGTGTCAC	656						
QY	965	TGCTGCCAGGCCCA	AGAACCTCATTTGATGCAGGTGTGATGCCCTGCGGGTGGGCATGGG	1024						
Db	655	TGCTGCCAGGCCCA	AGAACCTCATTTGATGCAGGTGTGATG--CTGCGGGTGGGCATGGG	598						
QY	1025	AAGTGGCTCCATCT	GCATTTATCCAGAAAGTGTGCGCTGTGGCGGGCCCCCAAGCAACAGC	1084						
Db	597	AAGTGGCTCCATCT	GCATTTATCCAGAAAGTGTGCGCTGTGGCGGGCCCCCAAGCAACAGC	538						
QY	1085	AGTGTACAAAGGT	GTATGAGTATGCACGGCGCTTTGGTGTCCGGTCATTTGCTGATGAGG	1144						
Db	537	AGTGTACAAAGGT	GTACAGATATGCACGGCGCTTTGGTGTCCGGTCATTTGCTGATGAGG	478						
QY	1145	AATCCAATAATGT	GGTCAATATTGCGAAAGCCTTGGCCCTTGGGGCCTCCACAGTCATGAT	1204						

Db 477 AATCCAAATGTGGCTCATATTTGCGAAGCCTTGCCCTTGCGGCTCACAGTCATGAT 418
QY 1205 GGGCTCTCTCCTGGCTGCCACCACTGAGCCCTGCTGTAATACTTCTTCCGATGGGAT 1264
Db 417 GGGCTCTCTCCTGGCTGCCACCACTGAGCCCTGCTGTAATACTTCTTCCGATGGGAT 358
QY 1265 CCGCTAAAGAAATATCGCGTATGGCTTCTCTCGATGCCATGAGCAAACACCTCAGCAG 1324
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QY 1385 TGTGACGACAAAGGGTCAATCCACAAATTTGTCCCTTACCTGATTCGGCATCCACA 1444
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QY 1505 GGAGCTTAAGTTTGAGACAGAACGCTCTCAGCCAGGTGGAAGTGGTGTCCATAGCCT 1564
Db 117 GGAGCTTAAGTTTGAGACAGAACGCTCTCAGCCAGGTGGAAGTGGTGTCCATAGCCT 58
QY 1565 CCATTCGTATGAGAGCGGCTTTCTGAAAAGGGATCCAGCACACCTCTTCGGTTT 1621
Db 57 CCATTCGTATGAGAGCGGCAATCTGAAAAGGGATCCAGCACACCTCTTCGGTTT 1

RESULT 5
AL535072 1065 bp mRNA linear EST 13-FEB-2001
LOCUS AL535072 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF007YL07 5
DEFINITION prime, mRNA sequence.
ACCESSION AL535072
VERSION AL535072.1 GI:12798565
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1065)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 91 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF007YL07"
/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 271 a 270 c 295 g 228 t 1 others
ORIGIN

Query Match 62.2%; Score 1028.8; DB 9; Length 1065;
Best Local Similarity 99.0%; Pred. No. 2.6e-293;
Matches 1055; Conservative 1; Mismatches 8; Indels 2; Gaps 2;
QY 16 TCGAGACAGCGCGGTGTCTCTGTGTGGCCATGGCCGACTACTGATTAGTGGGGCA 75
Db 1 TCGAGACAGCGCGGTGTCTCTGTGTGGCCATGGCCGACTACTGATTAGTGGGGCA 60
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Db 61 CGTCTAGTGCACAGACGAGCTCAACAGCAGCAGCTCTTCAACTGCGGAGACGGCC 120
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QY 196 ACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCA 255
Db 181 ACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCA 240
QY 256 TGGACACAGTCAACAGAGGCTGGGATGGCCATAGCAATGGCGCTTACAGCGGATTTGGCT 315
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Db 301 TCATCCACCACAACCTGTACACCTGAATTTCCAGGCCAATGAAGTTCGGAAGTGAAGAAT 360
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Db 361 ATGAACAGGGATTCATCACAGACCCTGTGTCTCAGCCCCAAGATCGCGGGATG 420
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QY 496 TGGGAGCGCGCTTGTGGGCATCATCTCTCCAGGGACATTTCTCAAGAGAGAGG 555
Db 481 TGGGAGCGCGCTTGTGGGCATCATCTCTCCAGGGACATTTCTCAAGAGAGAGG 540
QY 556 AACATGACTGTTTCTTGGAAGAGATTAAGCAAAAGAGGAAGCTGGTGTAGCCCCC 615
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QY 616 GCAGCATCAGCTGAAGGAGGCAAAATGAAATTTCTGACGCGCAGCAAGAGGAAGTTGC 675
Db 601 CAGGCATCAGCTGAAGGAGGCAAAATGAAATTTCTGACGCGCA -CAAGAAAGGAAGTTGC 659
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QY 976 CCAAGAACCTCATTTGATGACAGGTGTGCATGCCCTGCGGGT -GGGCATGGGAAGTGGCTCC 1034
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QY 1035 ATCTGCATATCCAGGAAGTCTGGCCCTGTGGCGGCGCCCAAGCAA 1080
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RESULT 6
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LOCUS AL539530 LTI_FL013_FBnr1 Homo sapiens cDNA clone CS0DF033YP03 5
DEFINITION prime, mRNA sequence.
ACCESSION AL539530
VERSION AL539530.1 GI:12868830
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1049)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/clone_lib="LTI_FL013_FBnr1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@life.techn.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 267 a 265 c 288 g 227 t 2 others
ORIGIN
Query Match 61.5%; Score 1017.6; DB 9; Length 1049;
Best Local Similarity 98.7%; Pred. No. 5.3e-290;
Matches 1034; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
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Db 361 GATTTCATCACAGACCCCTGTGGTCTCTCAGCCCCAAGATTCGGCTGCGGATGTTTGGAGG 420
QY 445 CCAAGGCCCGGCATGCTTCTGCGGTATCCCAATCACAGACACAGGCCGATGGGAGCC 504
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Db 421 CCAAGGCCCGGCATGCTTCTGCGGTATCCCAATCACAGACACAGGCCGATGGGAGCC 480
QY 505 GCTTGGTGGCATCATCTCTCCAGGAGCATTTGATTTTCTCAAGAGAGGAGACATGACT 564
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Db 481 GCTTGGTGGCATCATCTCTCCAGGACATTTGATTTTCTCAAGAGAGGACATGACT 540
QY 565 GTTCTTGAAGAGATTAATGACAAAGAGGAAAGACTTGGTGTAGCCCCCGCAGCATCA 624
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Db 541 GTTCTTGAAGAGATTAATGACAAAGAGGAAAGACTTGGTGTAGCCCCCGCAGCATCA 600
QY 625 CACTGAAGGAGGCAATGAATTTCTGACGGCAGACGAAGAAGGAAAGTTGCCAATTGTAA 684
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Db 601 CACTGAAGGAGGCAATGAATTTCTGACGGCAGACGAAGAAGGAAAGTTGCCAATTGTAA 660
QY 685 ATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGACCTGAAGAAGATCGGACT 744
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Db 661 ATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGACCTGAAGAAGATCGGACT 720
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QY 865 TGCATCTTCCAGGGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAGACA 924
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Db 841 TGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAGACA 900
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Db 901 AATACCTTAATCTCCAAGTCAATGGAAGCAATGTGTGCTGCTGCCAGGCCAAGAAC 960
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Db 1020 CGCAGGAAGTGTGGCYTGTGGGGGCC 1047

RESULT 7
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LOCUS AL551909
DEFINITION AL551909 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D106Y610 5
prime, mRNA sequence.
ACCESSION AL551909
VERSION AL551909.1 GI:12890302
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1011)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      261 a      255 c      275 g      218 t      2 others
ORIGIN
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Query Match      59.7%; Score 987; DB 9; Length 1011;
Best Local Similarity 99.0%; Pred.No. 6.1e-281;
Matches 1001; Conservative 2; Mismatches 7; Indels 1; Gaps 1;
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Db      61 CGTGCCAGACGACGACTCACACAGCAGCAGCTCTTCACTGCGGAGAGG GGCCTCACTTA 120
OY      143 CAATGACTTTCTCATTTCCCTGGGTACATGACTTCACTGCAGACCAG GTGACCTTGAC 202
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OY      323 CCACAACCTGTACACCTGAATTCACAGGCCAATGAAGTTGGAAGAA AAATATGAACA 382
Db      301 CCACAACCTGTACACCTGAATTCACAGGCCAATGAAGTTGGAAGAA AAATATGAACA 360
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OY      443 GGGCAAGGCGCGCATGGTTTCTGCGGTATCCCAATCACAGACAGGCG GATGGGAG 502
Db      421 GGGCAAGGCGCGCATGGTTTCTGCGGTATCCCAATCACAGACAGGCG GATGGGAG 480
OY      503 CCGCTTGGTGGCATCACTCTCCAGGGACATGATTTTCTCAAGAGG GAGGACATGA 562
Db      481 CCGCTTGGTGGCATCACTCTCCAGGGACATGATTTTCTCAAGAGG GAGGACATGA 540
OY      563 CTGTTTCTTGAAGAGATTAATGACAAGAGGGAAGACTTGGTGTAGC CCCCGCAGCAT 622
Db      541 CTGTTTCTTGAAGAGATTAATGACAAGAGGGAAGACTTGGTGTAGC CCCCGCAGCAT 600
OY      623 CACACTGAAGGAGCAATGAATTTCTGCAGCGCAGCAAGAAGGGAAT TTGCCCATTTGT 682
Db      601 CACACTGAAGGAGCAATGAATTTCTGCAGCGCAGCAAGAAGGGAAT TTGCCCATTTGT 660
OY      683 AAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGACAGACCTGA AAAGATCGGGA 742
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OY      743 CTACCCACTAGCCTCCAAGAATGCCACAAGAACAAGCTGCTGTGGGGC GCCATTGGCAC 802
Db      721 CTACCCACTAGCCTCCAAGAATGCCACAAGAACAAGCTGCTGTGGGGC GCCATTGGCAC 780
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OY      803 TCATGAGGATGACAGTATAGGCTGGACTTGTCTCGCCGACGCTGTGTGATGTAGTGGT 862
Db      781 TCATGAGGATGACAGTATAGGCTGGACTTGTCTCGCCGACGCTGTGTGATGTAGTGGT 840
OY      863 TTGGACTCTTCCAGGGAATTTCCATCTTCCAGATCATATGATCAAGTACATCAAGA 922
Db      841 TTGGACTCTTCCAGGGAATTTCCATCTTCCAGATCATATGATCAAGTACATCAAGA 900
OY      923 CAAATACCTTAATCTCCAGTCATTTGGAGGCAATGTGTCTGCTGCCCCAGGCCAAGAA 982
Db      901 CAAATACCTTAATCTCCAGTCATTTGGAGGCAATGTGTCTGCTGCCCCAGGCCAAGAA 960
OY      983 CCTCATTTGATGCAGGTGTGATGCCCCCTGGGGTGGGCAATGGGAGTGCGTC 1033
Db      961 CCTCATTTGATGCAGGTGTGATG-CTGCGGGTGGGCAATGGGAGTGGYCC 1010
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RESULT 8
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LOCUS
DEFINITION   AL514250 LTI_NFL006_PL2 Homo sapiens cDNA clone CLOBB006ZE01 5
prime, mRNA sequence.
ACCESSION   AL514250
VERSION     AL514250.1 GI:12777744
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1028)
AUTHORS    Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT     Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      265 a      260 c      278 g      224 t      1 others
ORIGIN
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Query Match      58.9%; Score 973.4; DB 9; Length 1028;
Best Local Similarity 99.2%; Pred.No. 6.6e-277;
Matches 999; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
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Db      1 CACGGCGGGTGTCTGTGTTGGCCATGGCCGACTACCTGATTAGTGGGGGCACTCTTA 60
OY      83 CGTGCCAGACGACGACTCACAGCAGCAGCTCTTCAACTGGGAGAGCGGCTCACTTA 142
Db      61 CGTGCCAGACGACGACTCACAGCAGCAGCTCTTCAACTGGGAGAGCGGCTCACTTA 120
OY      143 CAATGACTTTCATTTCCCTGGGTACATGACTTCACTGCAGACCAGGTGACCTGAC 202
Db      121 CAATGACTTTCATTTCCCTGGGTACATGACTTCACTGCAGACCAGGTGACCTGAC 180
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Db 301 CCACAACCTGTACACCTGTAATTCACAGGCCAATGAAGTTCGGAAGTGAAGAATATGACACA 360
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Db 421 GGGCAAGGGCCGGCATGGTTTCTGCGGTATCCCAATCACAGACAGAGCCGGATGGGAG 480
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Db 900 CAAATACCCCTAATCTCCAAGTCAATTGGAGGCAATGTGCTCACTGTGCCAGGCCAAGAA 959
QY 983 CCTCATTTGATGCAGGTGTGATGCCCCCTGCGGGTGGGCATGGGAAGTG 1029
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Db 960 CCTCATTTGATGCAGGTGTGATG-¹CCTGCGGGTGGGCATGGGAATTG 1005

RESULT 9
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LOCUS AL560269 LTI_FL011_BC1 Homo sapiens cDNA clone CS0DG007YK185 prime
DEFINITION , mRNA sequence.
ACCESSION AL560269
VERSION AL560269
KEYWORDS AL560269.1 GI:12906570
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 994)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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1..994
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/clone="CS0DG007YK18"
/clone_lib="LTI_FL011_BC1"
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/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Noli-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 255 a 252 c 268 g 216 t 3 others
ORIGIN
Query Match 58.0%; Score 959.4; DB 9; Length 994;
Best Local Similarity 98.2%; Pred. No. 9.2e-273;
Matches 977; Conservative 3; Mismatches 14; Indels 1; Gaps 1;
QY 23 CACGCGCGGTGCTCTGTGTGGCCATGGCCGACATCTGATTAGTGGGCGACGTCTTA 82
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Db 1 CACGCGCGGTGCTCTGTGTGGCCATGGCCGACATCTGATTAGTGGGCGACGTCTTA 60
QY 83 CGTGCCAGACGACGACTCACAGACAGCAGCTTCAACTGCGGAGACGGCCTCACCTA 142
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Db 61 CGTGCCAGACGACGACTCACAGACAGCAGCTTCAACTGCGGAGACGGCCTCACCTA 120
QY 143 CAATGACTTCTCATTTCTCCCTGGGTACATCGACTTCACTGCAGACCAAGTGCACCTGAC 202
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Db 121 CAATGACTTCTCATTTCTCCCTGGGTACATCGACTTCACTGCAGACCAAGTGCACCTGAC 180
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VERSION BM550826.1 GI:18787334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 1061)
NIH-MGC http://mgc.ncl.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1980 row: m column: 22
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BASE COUNT 268 a 254 c 298 g 237 t 4 others
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VERSION AL542763.1 GI:12875127
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 968)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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QY	634	AGGCAATGAAATTTCTGCAGCGCAGCAAGAAAGTTGCCCATTTGTAATGAAGATG	693
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QY	694	ATGAGCTTGTGGCCATCATTTGCCCGACAGACCTGAAGAAGATCGGGACTACCCACTAG	753
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QY	814	ACAAGTATAGGCTGGACTTGTCTGCCCGAGGCTGTTGATGTAGTGGTTTGACTCTT	873
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DEFINITION	AGENCOURT_7049427 NIH_MGC_107 Homo sapiens cdna IMAGE:5805460 5', mRNA sequence.		
ACCESSION	BQ278808		
VERSION	BQ278808.1	GI:20489016	
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ORGANISM	Homo sapiens		
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AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: ATCC cdna Library Preparation: Rubin Laboratory cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2044 row: 1 column: 05		

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BASE COUNT	252 a	240 c	291 g 236 t 1 others
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DEFINITION AGENCOURT_6924369 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5814016

ACCESSION BQ058198

VERSION BQ058198.1 GI:19817538

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1023)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2066 row: p column: 17
High quality sequence stop: 726.

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Best Local Similarity 95.1%; Pred. No. 4.1e-258;

Matches 961; Conservative 0; Mismatches 46; Indels 4; Gaps 2;

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Job time : 2260 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: February 13, 2003, 04:50:26 ; Search time: 39 Seconds

(without alignments)
387.779 Million cell updates/sec

Title: US-09-846-637C-4

Perfect score: 2619

Sequence: 1 MADYLISGTSYVPDDGLTA.....SSAQVEGVSLSHSYERLRF 514

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1210.5	46.2	371	US-09-212-247C-9	Sequence 9, Appli
4	865	33.0	494	US-09-134-001C-5024	Sequence 5024, Ap
5	407	15.5	151	US-09-212-247C-8	Sequence 8, Appli
6	336	12.8	333	US-09-134-001C-5204	Sequence 5204, Ap
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9	293	11.2	346	US-08-441-139-2	Sequence 3, Appli
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25	98.5	3.8	679	US-09-268-347-26	Sequence 26, Appli
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27	96	3.7	424	US-08-871-267A-23	Sequence 23, Appli

28	96	3.7	424	3	US-08-871-267B-31	Sequence 31, Appli
29	96	3.7	424	4	US-09-618-419-31	Sequence 31, Appli
30	96	3.7	424	4	US-09-163-674-23	Sequence 23, Appli
31	95.5	3.6	456	2	US-08-679-635A-6	Sequence 6, Appli
32	95.5	3.6	456	4	US-09-419-163-6	Sequence 6, Appli
33	94	3.6	1248	2	US-08-348-353-17	Sequence 17, Appli
34	94	3.6	1248	2	US-08-465-965-17	Sequence 17, Appli
35	94	3.6	1248	3	US-08-465-966-17	Sequence 17, Appli
36	93.5	3.6	530	3	US-09-222-817-12	Sequence 12, Appli
37	93.5	3.6	530	3	US-09-222-817-14	Sequence 14, Appli
38	93.5	3.6	530	4	US-09-222-786-12	Sequence 12, Appli
39	93.5	3.6	530	4	US-09-222-786-14	Sequence 14, Appli
40	93.5	3.6	1004	4	US-09-268-347-30	Sequence 30, Appli
41	93	3.6	894	1	US-08-117-362-4	Sequence 4, Appli
42	93	3.6	894	1	US-08-486-924-4	Sequence 4, Appli
43	92.5	3.5	1215	4	US-09-134-001C-5319	Sequence 5319, Ap
44	92.5	3.5	1805	4	US-09-004-838-92	Sequence 92, Appli
45	92	3.5	797	2	US-08-222-617A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-925-230-7
Sequence 7, Application US/08925230
Patent No. 6147194
GENERAL INFORMATION:
APPLICANT: Collart, Frank
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
TITLE OF INVENTION: AND GMP PRODUCTION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,230
FILING DATE: September 8, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,665,583
FILING DATE: 12-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-925-230-7
Query Match 99.5%; Score 2605; DB 4; Length 514;
Best Local Similarity 99.6%; Pred. No. 1.6e-250;
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 MADYLISGTSYVPDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSALTKKIT 60
|||||

Db 1 MADYLISGTSYVPPDDGLTAOQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMAALTGGIGIFIHNCPTPEFOANEVRKVKKYEQGFITDPVY 120
Db 61 LKTPLVSSPMDVTVEAGMAIAMAALTGGIGIFIHNCPTPEFOANEVRKVKKYEQGFITDPVY 120
QY 121 LSPKDRVRDVFPEAKARHGFCGIPITDTGRMGSRVLVGISSRDIDFLKEEHDCLFEIIMT 180
Db 121 LSPKDRVRDVFPEAKARHGFCGIPITDTGRMGSRVLVGISSRDIDFLKEEHDCLFEIIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVINEDEDEVAIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVINEDEDEVAIARTDLKKNRDYPLASKDA 240
QY 241 KQOLLGGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKIKDKYPNLQVI 300
Db 241 KQOLLGGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIQEVVLACGRPQATAVYKVEYARREGVP 360
Db 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIQEVVLACGRPQATAVYKVEYARREGVP 360
QY 361 VIADGGIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGGIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTOVR 480
Db 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTOVR 480
QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYERLRF 514
Db 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYERLRF 514

RESULT 2
US-08-925-230-8
; Sequence 8, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; APPLICANT: Huberman, Eliezer
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; TITLE OF INVENTION: AND GMP PRODUCTION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-925-230-8

Query Match 97.7%; Score 2559; DB 4; Length 514;
Best Local Similarity 98.1%; Pred. No. 6e-246;
Matches 504; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MADYLISGTSYVPPDDGLTAOQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60
Db 1 MADYLISGTSYVPPDDGLTAOQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMAALTGGIGIFIHNCPTPEFOANEVRKVKKYEQGFITDPVY 120
Db 61 LKTPLVSSPMDVTVEAGMAIAMAALTGGIGIFIHNCPTPEFOANEVRKVKKYEQGFITDPVY 120
QY 121 LSPKDRVRDVFPEAKARHGFCGIPITDTGRMGSRVLVGISSRDIDFLKEEHDCLFEIIMT 180
Db 121 LSPKDRVRDVFPEAKARHGFCGIPITDTGRMGSRVLVGISSRDIDFLKEEHDCLFEIIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVINEDEDEVAIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVINEDEDEVAIARTDLKKNRDYPLASKDA 240
QY 241 KQOLLGGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKIKDKYPNLQVI 300
Db 241 KQOLLGGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIQEVVLACGRPQATAVYKVEYARREGVP 360
Db 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIQEVVLACGRPQATAVYKVEYARREGVP 360
QY 361 VIADGGIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGGIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTOVR 480
Db 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTOVR 480
QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYERLRF 514
Db 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYERLRF 514

RESULT 3
US-09-212-247C-9
; Sequence 9, Application US/09212247C
; Patent No. 6391603
; GENERAL INFORMATION:
; APPLICANT: POMPEJUS, Markus; SUELBARGER, Harald; JOEFFKEN, Hans
; WOLFGANG; DOVAL, Jose Luis Revuelta; JIMENEZ, Alberto;
; and GARCIA, Maria Angeles Santos
; TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii
; and the use thereof in microbial riboflavin
; synthesis
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM AT-compatible, Pentium processor
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/212,247C

; FILING DATE: 16-Dec-1998
; CLASSIFICATION: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-212-247C-9

Query Match 46.2%; Score 1210.5; DB 4; Length 371;
Best Local Similarity 64.2%; Pred. No. 5.3e-112;
Matches 240; Conservative 59; Mismatches 66; Indels 9; Gaps 4;

QY 146 DTGRMGRVLVGIISRDIDFLKEEHDCLFEEIMTKREDLVVAPRSITLKEANEILQRSK 205
| | : | | | | | | | | | | : | | | | | : | | | | | : | | | | | : |
Db 1 DDGKPTGKLOGITTSRDIOFVEDE--TLIVSEIMTK--DVITGKQGINLEENAOILKNTK 56
QY 206 KGKLPVNEDELVAIARTDLKKNRDYPLASKDA-KKQLCGAIGTHEDDKYRLDLA 264
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 KGKLPVDEAGCLVSMLSRTDLMKNQSYPLASKSADTKQLCGAIGTHEDDRORLAMLV 116
QY 265 QAGVDVVLDSSQGSNIFQINMIKIKYKPNLOVIGNVVTAQAQNLIDAGVDALRVG 324
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 EAGLDVVVLDSSQGSNSVFQINMIKIKETFPDLOVIAGNVVTRQQAASLIHAGADGLRIG 176
QY 325 MGSGLICITQEVLAACGRPOATAVYKVEYARRFGVPVIADGGIQNVGHIAKALALGASTV 384
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 MGSGLICITQEVMAACGRPOGTAVYNTQFANQFVPCIADGGVQNIQHTKAIALGASTV 236
QY 385 MMSGLAATTEAPGEYFFESDGIRLKKYRGMGLDAMD---KHLSSQRYFSEADKIKVA 440
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 237 MMGMLAGTTESPEGEYFFRDGKRLKTYRGMGSIDAMQKTDVKGNAAISRYFSESCKLVLA 296
QY 441 QGVSGAVQDKGSIHKFVPLYLAGIQHSCODIGAKSLTOVRAMMYSGETLKEEKTSSAQVE 500
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 297 QGVTSVIDKGSIKKIYPILYNGLOHSCODIGVRSLSVEFREKVDGSGVRFEEFRTPSAQLF 356
QY 501 GGVHSLHSYEKRLF 514
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 357 GGVHNLHSYEKRLF 370

RESULT 4
US-09-134-001C-5024
; Sequence 5024, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5024
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5024

Query Match 33.0%; Score 865; DB 4; Length 494;
Best Local Similarity 40.8%; Pred. No. 2e-77;
Matches 198; Conservative 95; Mismatches 170; Indels 22; Gaps 10;
QY 28 DGLTYNDLILPGYIDFTADVLTSLTKKITLKTPLVSSPMDTVTRAGMAIAMALTGG 87
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 ESTFDVLLIPASADVLPSPDVLKSLSDKIKLINIPVISAGMDTVTRSSKMAIAMAROGG 74

QY 88 IGFHHNCTPEFOANEVRKKVKEQGFITDPVVLSPKDRVVDVEEAKA---RHGFCGIP1 144
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 LGVIHKNMGVEEQADEVQKVRSENCVINSPPFLTPEE---SVYEAEALMGKYRISCVPI 131
QY 145 TDTGRMGRVLVGIISRDIDFLKEEHDCLFEEIMTKREDLVVAPRSITLKEANEILQRS 204
| | : | | | | | | | | | | : | | | | | : | | | | | : | | | | | : |
Db 132 VD-NQEDRKILGILTRDLRFI--EDFSIKISDVMTK-DNLITAPVGTTEDEAEAILQKH 187
QY 205 KGKLPVNEDELVAIARTDLKKNRDYPLASKDAKKQLCGAIGTHEDDKYRLDLA 264
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 188 KIEKLPLV-ENGRLEGLITIKDIEKYLEFPYAAKDEHGRLLAAAICTSKDTEIRAQKLV 246
QY 265 QAGVDVVLDSSQGSNIFQINMIKIKYKPNLOVIGNVVTAQAQNLIDAGVDALRVG 324
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 247 EAGVDALIDTAHAGHSKGVINQVKHIKETPEITVAVGNVATAEATRALFEAGADVVKVG 306
QY 325 MGSGLICITQEVLAACGRPOATAVYKVEYARRFGVPVIADGGIQNVGHIAKALALGASTV 384
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 307 IGPGLITTRVYVAGVGPQITVAVYDCATEARKHGKAILADGGIKFSGDIKALAAAGHAV 366
QY 385 MMSGLAATTEAPGEYFFESDGIRLKKYRGMGLDAMDKHLSSQNRYSSEADKIK--VAQ 441
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 367 MLGSLAGTESPGATEVFQGRQYKYYRGMGLGAMEK--GSNDRYFQE-DKTPRKFTVE 423
QY 442 GVSAGVQDKGSIHKFVPLYLAGIQHSCODIGAKSLTOVRAMMYSGETLKEEKTSSAQVEG 501
| | : | | | | | | | | | | : | | | | | : | | | | | : | | | | | : |
Db 424 GIEGRTAYKGLQDTIYQIMGVRAGMGVYTGSENLLKRLRE----EAQFTRMGPAGLAES 478
QY 502 GGVHSL 506
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 479 HPHNV 483

RESULT 5
US-09-212-247C-8
; Sequence 8, Application US/09212247C
; Patent No. 6391603
; GENERAL INFORMATION:
; APPLICANT: FOMPEJUS, Markus; SUELBERGER, Harald; JOEFFKEN, Hans
; and GARCIA, Maria Angeles Santos
; TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii
; and the use thereof in microbial riboflavin
; synthesis
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM AT-compatible, Pentium processor
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/212,247C
; FILING DATE: 16-Dec-1998
; CLASSIFICATION: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-212-247C-8
Query Match 15.5%; Score 407; DB 4; Length 151;
Best Local Similarity 61.3%; Pred. No. 1.1e-32;

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Matches 84; Conservative 11; Mismatches 40; Indels 2; Gaps 1;
QY 11 SYVPDDGLTAQOLF--CGDGLTYNDLFLPGYIDFTADQVDLTSLTKKTLKTPLYSS 68
:| | | | | :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 TYAEKDGLSVEQMDSKTRGGLTYNDLFLPGKIDFPSSEVLSSRLTKKTLNAPFVSS 74
QY 69 PMDTVTEAGMAIAMALTGGIGFIHNCTPEEQANEVRKVKKYEQGITDPVLSPKDRVR 128
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 PMDTVTEADMAIHMAALLGGIGIIHNCTAEQAEWVRVKKYENGFINAPVVGPDATVA 134
QY 129 DVFEAKARHGFCGIPIT 145
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 135 DVRRMKNEFGFAGFPVT 151

RESULT 6
US-09-134-001C-5204
; Sequence 5204, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5204
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5204

Query Match 12.8%; Score 336; DB 4; Length 333;
Best Local Similarity 31.2%; Pred. No. 4.6e-25;
Matches 101; Conservative 53; Mismatches 130; Indels 40; Gaps 8;
QY 183 EDLVVAPRSITLKEANEILQRSKKG-----KLPIVNE-----DDELVAIARTDL----- 227
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 15 EDIQLIPNKCIVESRSECTSVKFGPRTFKLPVVPANMOTVMNEELAQWFAENDYFYIMH 74
QY 228 ---KKNRDYPLASKDAKKQLLGAIGTHEDDKYRLDLLAQAGV--DYVVLDSQGSNIF 282
:| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 75 RFNEENR-IPFTKKMHHAAGLFASISVGVKENEENFIEKLASSSLIPEYITIDIAHGSNS 133
QY 283 QINMIKIKDKYPNLQVIGNVVTAQAQAKNLIDAGVDALRVGMSGISICI--IQEVLACG 340
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 134 VINMIKHIKHLPNSEFVIAGNVGTPEGVRELENAGADATKVGIGPRVCITIKITGFGTG 193
QY 341 RPQATAVYKVEYARRFGVPVIADGCIQNVGHIAKALALGASTVMGSLAATTEAPGEY 400
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 194 GWQLSALNLCNKAARK--PIADGILRTHGDIAKSIRFGATVMVIGSLFAAHEESPGET 250
QY 401 FFSDGIRLKKYRGMGSLDAMDKHLSSQNRYFSEADKIKVAQVSGAVQDKGSIHKFPYL 460
| | : | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 251 VELDGKKYKEFGSASEYQKEH-----KNVEGKKMFVEHKGSLKDTLTLEM 296
QY 461 IAGIQHSCQDIGAASLTQVRAMY 484
:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 297 EQDLQSSISYAGGKDLKSLRTVDY 320

RESULT 7
US-08-774-169-1
; Sequence 1, Application US/08774169
; Patent No. 5756332
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL GUANOSINE MONOPHOSPHATE REDUCTASE
```

```
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,169
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0182 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
US-08-774-169-1

Query Match 12.7%; Score 331.5; DB 1; Length 366;
Best Local Similarity 26.9%; Pred. No. 1.5e-24;
Matches 95; Conservative 73; Mismatches 138; Indels 47; Gaps 10;
QY 183 EDLVVAPRSITLKEANEI-----LQRSKK--GKLPIV--NEDD----ELVAIARTDL 227
:| | : | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 31 KDVLRLPKRSTLLKSRSEVDLTRSFSPNSKQTYSGVPIIAANMDTVGFEMAKVLCFSL 90
QY 228 --KKNRDYPLA-----SKDAKKQLLGAIGTHEDDKYRLDLLAQ--GVDVVVLDS 275
:| | : | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 91 FTAVHKHYSLVQWQEFAGQNPDCLEHL--AASSGTGSSDFEQLEQLLEAIPQVKYICLDV 148
QY 276 SQGNSIFQINMIKIKDKYPNLQVIGNVVTAQAQAKNLIDAGVDALRVGMSGISICIQE 335
: | | : : | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 149 ANGYSEHFVEFVKDVRKRFPOHTIMAGNVVTGEMVEELLISGADITIKVGIGSVCTTRK 208
QY 336 VLAGRPQATAVYKVEYARRFGVPVIADGCIQNVGHIAKALALGASTVMGSLAATTE 395
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 209 KTGVGYPQLSAVMECADAHAHGLKGHITSDGCCSPGDVAKAFGAGADFVMLGMLAGHSE 268
QY 396 APGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNRYFSEADKIKVAQVSGAVQDKGSIHK 455
: | | | | : | : | : | | | : | : | : | : | : | : | : | : | : |
Db 269 SGGELIERDGKKYKLFYGMSSSEMAKKYAGVAEY-----RASEGKTVEVPFKGDVEH 321
QY 456 FVPYLIAGIQHSCQDIGAASLTQVRAMYSGELKFEKRTSSAQVEGCVHSLHS 508
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 322 TIRDILGTRSTCTYVGAAKIKEL-----SRRTTFIRVTQOVNPIFS 363

RESULT 8
US-08-774-169-4
; Sequence 4, Application US/08774169
; Patent No. 5756332
; GENERAL INFORMATION:
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Db 337 EQENRIE 343

RESULT 10
US-08-441-139-2

; Sequence 2, Application US/08441139
; Patent No. 5773245

; GENERAL INFORMATION:

; APPLICANT: Wiltrop, Dr. Karl D.

; APPLICANT: Robinson, Anne S.

; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF

; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: NY

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/441,139

; FILING DATE: 15-MAY-1995

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/089,997

; FILING DATE: 06-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Digilio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8646

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 682 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-441-139-2

Query Match 4.5%; Score 117.5; DB 1; Length 682;
Best Local Similarity 20.8%; Pred. No. 0.0082;

Matches 83; Conservative 58; Mismatches 129; Indels 129; Gaps 20;

QY 127 VRDVFEA-KARHGFPGIPITDTGRMGRVGLIISRDIIDFLKEE-----EHDCE-- 174

Db 283 VRQLKAFKKKH---GIDVSDNNKALAKL-----KRAEAKAKKALSSQMSSTRIEIDSFVD 334

QY 175 ---LEEIMT--KREDLVVAPRSITLKEANEILQRSKKKGLPIVNEDELVAIIARTDLKK 229

Db 335 GIDLSETLTRAKFEELNLDLFKKTLKPYEKVLQDSGLEKKDV---DDIVLVGSTRIPK 390

QY 230 NRDYPLASKDAKKQLLGAIGTGHEDDKYRLDLAQAQV-----DYYVLDSQGSNSI 281

Db 391 VOQLLESYFDGKR---ASKGINPDEAVAYGAAYQAAGVLSGEEGVEDIIVLLD----- 438

QY 282 FOINMIKIKDKKYPNLQVIGG-----NVVTAQAQAKNLIDAGVDALRVGMGSGSICII 333

Db 439 --VNALTL-----GIETTGCVMTPLIKRNTAIPTKKSQIFSTAVD----- 476

QY 334 QEVLAGCRQAATAVYKVEYARF-----GVPVIADGGIONVGHIAKALALG 380

Db 477 -----NQPTVMIKVYEGERAMSKDNNLIGKFEELTGIPAPRG---VPQIEVTFALD 524

QY 381 ASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNRFFSEADKIKVA 440

Db 525 ANGIK---VSATDKGTGK---SESTITNDKGRLTQEIDRMVEAEKFASEDASIK-- 576

QY 441 QGVSGAVQDKGSIHKFVPLYLAGIQHSCQ-----DIGAK 474

Db 577 ----AKVESRKNLENYA-----HSLKNQVNGDLGEK 603

RESULT 11

US-09-134-001C-4675

; Sequence 4675, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucelte-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4675

; LENGTH: 691

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

; US-09-134-001C-4675

Query Match 4.2%; Score 109.5; DB 4; Length 691;

Best Local Similarity 20.0%; Pred. No. 0.053;

Matches 90; Conservative 64; Mismatches 137; Indels 159; Gaps 21;

QY 92 HHNCTPEFQANEYRKVKYEQGFITDPVVLSPKDRVDFEAKARHGFPGIPITDTGRMG 151

Db 299 HLQSTKNFVREBLKTRRFLNDIITQNYAIAPYODIR-----FLIYP-QDLPKHE 347

QY 152 SRLVGITSSRDIDFLKEEHDFLEETMKREDLVVAPRSITLKEANEI----LQRSKK 206

Db 348 KK-----NSSQIDYIPDFVLEQLFEHINDLHKDLIPVW-WIAFKTGRLISDVLTLQNMCL 401

QY 207 GKLPVNEDELVAIIARTDLKKNRDYPLASKDAKKQLLGAIGTGHEDDKYRLDLAQA 266

Db 402 AK---VNGKYSITTDIAKTFVKGHR-IPIDNKLA-----DIIA-- 435

QY 267 GVDVVVLDSQGSNSIFQINMIKIKDKKYPN-----LQVIGNVVTAQAQ 309

Db 436 ---VLIADSKS-----KSTKDNPNNNYIFAIIYKGRKGMPTQHMVRAHLNHLISK 482

QY 310 AKNLIDAGVD-----ALRVGMGSGSICIIQEVLAGCRQAATAVY-KVEYAR 355

Db 483 TKNIIDEQGEIFHFKTHQFRHTYAVKLNGCADILTIQELLAHSSPEMTLRYAKLLDPTK 542

QY 356 RFGVPVI-----ADGGIQNVGHIA---KAL-----ALGASTVMGSLAATY- 394

Db 543 RKAFTESVIDOGAFSFDVDGKIKNIQHSSELSEKALNSLWQEHKLNAMDNPYGTCHARLSG 602

QY 395 ----EAPG-----EYFSDGIRLKKY-----RGMGSLDAMDK 422

Db 603 DCPYMEAPPCPLTNCNGKPKCKDLAIGFSD-LDVEKYEHLHIKSTVKSIELAKNNNRQDMVEK 661

QY 423 HLSSQNR-----FSEADKIKV 439

Db 662 HINILNKYEELTGNIKDGNIIFFGRSNRIKV 691

RESULT 12

US-09-134-001C-3866

; Sequence 3866, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucelte-Stamm et al


```

; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-139-7

Query Match          3.9%; Score 102.5; DB 1; Length 663;
Best Local Similarity 20.2%; Pred. No. 0.24;
Matches 107; Conservative 78; Mismatches 227; Indels 117; Gaps 23;

QY 37 ILPGYIDFTADQ-----VDLTSALTKKITLKT--PLVSSPMDTVT 74
Db 68 ITPSYAFTEDERLVGEAAKNQAPSNPENTIFDIKRLIGRKFDEKTMAKDIKSFPHIYN 127
QY 75 EAGMAIAMALLTGIGIFIHNCPT-EFOANEVRKVKKYEQGFITDPVVLSPKDRVDFEEA 133
Db 128 DKNRPLVEVNVGG---KKKKFTPEEISAMILSKMKQTAEAYLGPVT----- 171
QY 134 KARHFCGIP--ITDTGRMGSRVLGIISRDIIDFLKEEHDCFLIEIMTKRE----- 183
Db 172 ---HSVVTVPAYFNDAQRQATKAGTIAGLNVRIVNEPTAAAIAYGLDKTDTEKHIVVY 228
QY 184 DLVVAPRSITLKEAN---EILQSKKKGLPIVNEDELVAIARTDLKKNRDYPLASKD 239
Db 229 DLGGTFDVSLSLIDNGVFVLAATSGDTHLGGEDFDNRVINYLAITYNRKN-----NVD 282
QY 240 AKKQLLGAAG--THEDKRYRLDLAQAGVDVVLDSQGSNFIQ-INMIKYIKDKYPN 296
Db 283 VTKDL---KAMGKLKREVEKANGTSSQSVRIEIESFNGQDFSETLSRAKFEEIKHGS 339
QY 297 LQVIGNVVTAQAQKNLIDAGVDALRVGMSSGSIQIEVLAC--GRPQATAVYK----V 350
Db 340 LQEDFEFEVQVLKDSNLKSEIDILVLVGSGSTRIPKVQELLESEFGKKASKGINPEAVA 399
QY 351 YEYARRFGVPVIADGQIONVGH-AKALALGASTV--MMGSLAATTEAP--GEYFFSDG 405
Db 400 YGAIVQAGV-LSGEEGSDNIVLDDVILPTLGIEFTGGVMTKLIGRNTPIPTRKSSQIFSTA 458
QY 406 IRLKRYRGMGLDAMDKHLSSQNRYSFSEADKIKVAQGVSGAVQDKGSIHKE---VPYLI 461
Db 459 V-----DMQNTVL-----IQVEGERTLTKDNNLLGKFDLRGIPAP 495
QY 462 AGIQ--HSCQDIGAKSLTQVRAMMYSGELKFEK-----RTSSAQVE 500
Db 496 RGVPGIEVTFEVDANGVLTVSAVDKSGKPEKLVIKNDKGRLEEDIE 544

RESULT 15
US-09-066-047-8
; Sequence 8, Application US/09066047A
; Patent No. 6306394
; GENERAL INFORMATION:
; APPLICANT: MURPHY, Cheryl
; STOREY, James
; BELTZ, Gerald A.
; COUGHLIN, Richard T.
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF
; USE OF GRANULOCYTIC ERLICHIA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
```

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; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,047A
; FILING DATE: 24-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,869
; FILING DATE: 25-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 106.941.156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-066-047-8

Query Match          3.9%; Score 102; DB 4; Length 420;
Best Local Similarity 21.3%; Pred. No. 0.13;
Matches 85; Conservative 65; Mismatches 103; Indels 146; Gaps 23;

QY 158 ISSRIDFLKEE-----EHDCFLIEIMTK--REDLV--VAPRSITLKEANEI 200
Db 22 ISSKFDLVIEDITQALLDADVNLGVDEFIENVKSKIYGVGDVYKGLPEQMVIRIEEC 81
QY 201 L-----QRSK---KGKLPi-----VNEDELVAIARTDLKKNRDYPL----- 235
Db 82 LIEVLGNEKSALDLKGIPAVIMWGLQGVGKTTNTYKVALR--LKKDSKNPLVASLDYV 139
QY 236 --ASKDAKKQLLGAAGTHTHE--DDKYRLDLLAQ-----GVDVVVLDSQGSNFIQ- 283
Db 140 RPARAEQLKVLADGVGIDSLPIVEEQKPLDIAKRAMREARLKGHDVLLDTAGRLHINQD 199
QY 284 -INMIKYIKDKYPNLQVIGNVVTAQAQKNLIDAGVDALRVGMSSGSIQIE----- 335
Db 200 MIDEKCVKKEVSPAETV-----LV--VDSL---MGQDAVTMVRKFNEELGI 241
QY 336 -----VLACGRPOATAVYKRYEYARRFGVPV--IADG-----GIQNVGH 372
Db 242 TGTIFTRADGDPRGAILSMKLV---GCPIKFMSTGEKPEDLDIFYPDRIARRMLNMGD 298
QY 373 IAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNRYS 432
Db 299 VA-----SLVEKAVEAVGKDTINE-LQAKAKKGKFDLDDLVIQLKALNK--- 341
QY 433 EADKIKVAQGVSGAVQDKGSIHKEFVPL-----IAGI 464
Db 342 -----MGI---ANIMKFIIPAFGNDIKRKVAGI 366
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Search completed: February 13, 2003, 06:34:39
Job time : 43 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 06:32:42 ; Search time 04 Seconds
(without alignments)
43.198 Million cell updates/sec

Title: US-09-846-637C-4
Perfect score: 2619
Sequence: 1 MADYLISGTSYVPDDGLTA.....SSAQVEGVHILHSYEKRLF 514

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2605	99.5	514	10	US-09-853-918-63 Sequence 63, Appl
2	2595	99.1	514	10	US-09-853-918-49 Sequence 49, Appl
3	2234	85.3	514	10	US-09-853-918-62 Sequence 62, Appl
4	2222	84.8	514	10	US-09-853-918-48 Sequence 48, Appl
5	2202	84.1	514	10	US-09-853-918-64 Sequence 64, Appl
6	2201	84.0	514	10	US-09-853-918-65 Sequence 65, Appl
7	1862	71.1	384	10	US-09-853-918-20 Sequence 34, Appl
8	1861.5	71.1	385	10	US-09-853-918-34 Sequence 34, Appl
9	1860.5	71.0	385	10	US-09-853-918-32 Sequence 32, Appl
10	1860	71.0	384	10	US-09-853-918-29 Sequence 32, Appl
11	1859.5	71.0	385	10	US-09-853-918-36 Sequence 36, Appl
12	1858	70.9	384	10	US-09-853-918-24 Sequence 24, Appl
13	1857.5	70.9	385	10	US-09-853-918-37 Sequence 37, Appl
14	1857.5	70.9	385	10	US-09-853-918-38 Sequence 38, Appl
15	1857	70.9	384	10	US-09-853-918-22 Sequence 22, Appl
16	1856	70.9	384	10	US-09-853-918-21 Sequence 21, Appl
17	1856	70.9	384	10	US-09-853-918-25 Sequence 25, Appl
18	1856	70.9	384	10	US-09-853-918-27 Sequence 27, Appl
19	1855.5	70.8	385	10	US-09-853-918-31 Sequence 31, Appl

20	1855.5	70.8	385	10	US-09-853-918-33	Sequence 33, Appl
21	1855.5	70.8	385	10	US-09-853-918-35	Sequence 35, Appl
22	1855	70.8	384	10	US-09-853-918-23	Sequence 23, Appl
23	1853	70.8	384	10	US-09-853-918-28	Sequence 28, Appl
24	1852	70.7	384	10	US-09-853-918-26	Sequence 26, Appl
25	1851.5	70.7	385	10	US-09-853-918-39	Sequence 39, Appl
26	1644	62.8	384	10	US-09-853-918-30	Sequence 30, Appl
27	1210.5	46.2	371	9	US-10-076-157-9	Sequence 9, Appl
28	875	33.4	489	10	US-09-815-242-11953	Sequence 11953, A
29	874.5	33.4	217	10	US-09-925-302-829	Sequence 829, App
30	863	33.0	506	9	US-09-738-626-4172	Sequence 4172, Ap
31	836	31.9	488	10	US-09-815-242-10986	Sequence 10986, A
32	521	19.9	133	10	US-09-853-918-61	Sequence 61, Appl
33	492	18.8	477	9	US-09-738-626-6445	Sequence 6445, Ap
34	425.5	16.2	156	10	US-09-734-017A-76	Sequence 76, Appl
35	407	15.5	151	9	US-10-076-157-8	Sequence 8, Appl
36	317	12.1	325	10	US-09-815-242-12738	Sequence 12738, A
37	317	12.1	325	10	US-09-815-242-13055	Sequence 13055, A
38	316	12.1	325	10	US-09-815-242-10811	Sequence 10811, A
39	316	12.1	327	10	US-09-815-242-4895	Sequence 4895, Ap
40	312	11.9	325	10	US-09-815-242-11543	Sequence 11543, A
41	303.5	11.6	347	10	US-09-815-242-10035	Sequence 10035, A
42	302.5	11.6	347	10	US-09-815-242-13914	Sequence 13914, A
43	283	10.8	328	10	US-09-815-242-13261	Sequence 13261, A
44	173.5	6.6	265	10	US-09-925-300-1572	Sequence 1572, Ap
45	154	5.9	374	9	US-09-738-626-4174	Sequence 4174, Ap

ALIGNMENTS

RESULT 1
US-09-853-918-63
Sequence 63, Application US/09853918
Patent No. US20020068346A1
GENERAL INFORMATION:
APPLICANT: Kyrestek, Stanley R.
APPLICANT: Sherliff, Steven
APPLICANT: Witmer, Mark R.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Mouravieff, Julie E.
APPLICANT: Einspahr, Howard M.
APPLICANT: Kish, Kevin
TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
FILE REFERENCE: DE24NP
CURRENT APPLICATION NUMBER: US/09/853,918
PRIOR APPLICATION NUMBER: 2001-05-10
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 514
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Collart, Frank R.
TITLES: Cloning and Sequence Analysis of the Human and Chinese
TITLE: Hamster Inosine-5'-monophosphate Dehydrogenase cDNAs
JOURNAL: J. Biol. Chem.
VOLUME: 263
ISSUE: 30
PAGES: 15769-15772
DATE: 1988-10-25
US-09-853-918-63

Query Match 99.5%; Score 2605; DB 10; Length 514;
Best Local Similarity 99.6%; Pred. No. 2.3e-211;
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MADYLIISGGTSTYVPDDGLTAQOLFNCNGDGLTYNDFLILPGYIDFTADQYDLTSALTKKIT	60
Db	1	MADYLIISGGTSTYVPDDGLTAQOLFNCNGDGLTYNDFLILPGYIDFTADQYDLTSALTKKIT	60
QY	61	LKTPLVSSPMDTVT EAGMAIAMAALTGGIGIFIHNCTPEFOANEVRKVKYEQGFIITDPV	120
Db	61	LKTPLVSSPMDTVT EAGMAIAMAALTGGIGIFIHNCTPEFOANEVRKVKYEQGFIITDPV	120
QY	121	LSPKDRVRDVF EAKARHGF CGIPITDTGRMGSRVLGIISSRIDIDFLKEEHDCFL EIMT	180
Db	121	LSPKDRVRDVF EAKARHGF CGIPITDTGRMGSRVLGIISSRIDIDFLKEEHDCFL EIMT	180
QY	181	KREDLVAPRSITLKEANEILORSKKGLPIVNEDELVAI IARTDLKKNRDPYASKDA	240
Db	181	KREDLVAPRSITLKEANEILORSKKGLPIVNEDELVAI IARTDLKKNRDPYASKDA	240
QY	241	KKOLLGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIKYIKDKYPNLQVI	300
Db	241	KKOLLGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIKYIKDKYPNLQVI	300
QY	301	GGNVYTTAAQAKN LIDAGVDALRVGMSSSICIIOEVLACGRPQATAVYKYEYARFGVP	360
Db	301	GGNVYTTAAQAKN LIDAGVDALRVGMSSSICITQEV LACGRPQATAVYKYSEYARFGVP	360
QY	361	VIADGGIQNVGHI AKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
Db	361	VIADGGIQNVGHI AKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
QY	421	DKHLSSQNRYFSEADKIKVAQGVSGAVODKGSIHKFVPLYIAGIQHSCODIGAKSLTQVR	480
Db	421	DKHLSSQNRYFSEADKIKVAQGVSGAVODKGSIHKFVPLYIAGIQHSCODIGAKSLTQVR	480
QY	481	AMMYSGELKF EKR TSSAQVEGGVHSLHSY EKR LF 514	
Db	481	AMMYSGELKF EKR TSSAQVEGGVHSLHSY EKR LF 514	

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RESULT 2
US-09-853-918-49
: Sequence 49, Application US/09853918
: Patent No. US20020068346A1
:
: GENERAL INFORMATION:
: APPLICANT: Krystek, Stanley R.
: APPLICANT: Sheriff, Steven
: APPLICANT: Wiltner, Mark R.
: APPLICANT: Hollenbaugh, Diane L.
: APPLICANT: Yan, Ning
: APPLICANT: Mouravieff, Julie E.
: APPLICANT: Einspahr, Howard M.
: APPLICANT: Kish, Kevin
: TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
: FILE REFERENCE: DB24NP
: CURRENT APPLICATION NUMBER: US/09/853,918
: CURRENT FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: 60/203,448
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 49
:
: LENGTH: 514
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
US-09-853-918-49

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Query Match	99.18;	Score 2595;	DB 10;	length 514;
Best Local Similarity	99.28;	Pred. No. 1.6e-210;		
Matches 510; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

QY	61	LKPLVSSPMDVTVEAGMAIAMALTGGIGIFIHNNCTPEFQANEVRKVKYKEOGFITDPVV	120
Db	61	LKTPLVSSPMDVTVEAGMAIAMALTGGIGIFIHNNCTPEFQANEVRKVKYKEOGFITDPVV	120
QY	121	LSPKDRVRDVEEAKARHGFCCGIPITDTGRMGSRLVGIISSRDIDFLKEEHDCLFEEIMT	180
Db	121	LSPKDRVRDVEEAKARHGFCCGIPITDTGRMGSRLVGIISSRDIDFLKEEHDCLFEEIMT	180
QY	181	KREDLVAPRSITLKEANEILQRSKKGLPIVNEDEDELVAIARTDLKKNRDYPLASKDA	240
Db	181	KREDLVAPAGITLKEANEILQRSKKGLPIVNEDEDELVAIARTDLKKNRDYPLASKDA	240
QY	241	KKOLLGGAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQIINMIKYLKDKYPNLQVI	300
Db	241	KKOLLGGAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQIINMIKYLKDKYPNLQVI	300
QY	301	GGNVVTAQAQAKNLIDAGVDALRVGMSSGSIICIIQEVLAGCRPQATAVYKVEYARREGVP	360
Db	301	GGNVVTAQAQAKNLIDAGVDALRVGMSSGSIICIIQEVLAGCRPQATAVYKVEYARREGVP	360
QY	361	V1ADGCIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
Db	361	V1ADGCIQNVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
QY	421	DKHLSSQNRIFYSEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR	480
Db	421	DKHLSSQNRIFYSEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR	480
QY	481	AMMYSGELKEFKRTSSAQVEGGVHLSHSYEKRLF 514	
Db	481	AMMYSGELKEFKRTSSAQVEGGVHLSHSYEKRLF 514	

```

RESULT 3
US-09-853-918-62
; Sequence 62, Application US/09853918
; Patent No. US20020068346A1
;
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sherliff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
;
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
;
; FILE REFERENCE: DB24NP
;
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 62

```

```

; ORGANISM: Homo sapiens
;
; PUBLICATION INFORMATION:
;
; AUTHORS: Gu, Jing Jin
;
; AUTHORS: Spychala, Jozef
;
; AUTHORS: Mitchell, Beverly S.
;
; TITLE: Regulation of the Human Inosine Monophosphate
;
; TITLE: Dehydrogenase Type I Gene
;
; JOURNAL: J. Biol. Chem.

```

PAGES: 4458-4466
DATE: 1997-02-14
US-09-853-918-62

Query Match 85.3%; Score 2234; DB 10; Length 514;

Best Local Similarity 83.58; Pred. No. 3.8e-180;
Matches 429; Conservative 39; Mismatches 46; Indels 0; Gaps 0;

QY	1	MADYLI	SGT	SYVP	DDGLT	AOQLE	NC	GDGLTY	ND	FL	PG	YID	TADQ	LD	T	S	A	L	T	K	R	I	T	60	
Db	1	MADYLI	SGT	GYVP	EDGLT	AOQLE	F	A	S	A	D	G	L	T	Y	N	D	F	L	I	B	E	F	I	60
QY	61	LKTP	LV	SSP	MDTV	TE	A	G	M	A	I	A	M	A	L	T	G	G	I	G	F	I	H	N	120
Db	61	LKTP	LV	ISSP	MDTV	TE	A	D	M	A	I	A	M	A	L	M	G	G	I	G	F	I	H	N	120
QY	121	LSPK	DR	RV	DV	F	E	A	K	A	R	H	G	F	C	G	P	I	T	D	T	G	R	M	180
Db	121	LSP	SH	V	G	D	V	L	E	A	K	M	R	H	G	F	S	G	P	I	T	E	T	G	180
QY	181	KRED	LV	AP	RS	IT	L	K	E	A	N	E	I	L	O	R	S	K	K	G	K	L	P	I	240
Db	181	PRIE	LV	AP	AG	VT	L	K	E	A	N	E	I	L	O	R	S	K	K	G	K	L	P	I	240
QY	241	KKOL	L	G	A	I	G	T	H	E	D	K	Y	R	L	D	L	A	Q	A	G	V	D	V	300
Db	241	QKOL	L	G	A	I	G	A	V	G	T	R	E	D	K	Y	R	L	D	L	L	T	Q	A	300
QY	301	G	N	V	T	A	A	O	A	K	N	L	I	D	A	G	V	D	L	R	V	G	M	G	360
Db	301	G	N	V	T	A	A	O	A	K	N	L	I	D	A	G	V	D	L	R	V	G	M	G	360
QY	361	V	I	A	D	G	I	O	N	V	G	H	I	A	K	A	L	A	L	A	L	A	L	A	420
Db	361	I	A																						

```

RESULT 4
US-09-853-918-48
: Sequence 48, Application US/098533918
: Patent No. US20020068346A1
: GENERAL INFORMATION:
: APPLICANT: Krystek, Stanley R.
: APPLICANT: Sheriff, Steven
: APPLICANT: Wilmer, Mark R.
: APPLICANT: Hollenbaugh, Diane L.
: APPLICANT: Yan, Ning
: APPLICANT: Mouravieff, Julie E.
: APPLICANT: Einspahr, Howard M.
: APPLICANT: Kish, Kevin
: TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
: FILE REFERENCE: DB24NP
: CURRENT APPLICATION NUMBER: US/09/853,918
: CURRENT FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: 60/203,448
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 48
: LENGTH: 514
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-853-918-48

```

Query Match	84.8%;	Score 2222;	DB 10;	Length 514;
Best Local Similarity	83.1%;	Pred. No. 3.9e-179;		
Matches 427;	Conservative 39;	Mismatches 48;	Indels 0;	Gaps 0;
1	MADYLLISGGTSTYVDDGLTAQQLFNCGGDGLTYNDFILPGYIDFTADDVLTSLATKKIT	60		

```
Db      ||||| | | : | | | | | | | | | | | | | | | | | | | | | | | |
1 MADYLISSGCTGYVPEDGLTAQQLFASADDELTYNDFLILPGFIIDEVDLTSLTRKIT 60
```

[illegible]

```

RESULT 5
US-09-853-918-64
; Sequence 64, Application US/09853918
; Patent No. US2002068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DH24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64

```

```

? ORGANISM: Homo sapiens
?
? PUBLICATION INFORMATION:
?
? AUTHORS: Dayton, Jennifer S.
?
? AUTHORS: Lindsten, Tullia
?
? AUTHORS: Thompson, Craig B.
?
? AUTHORS: Mitchell, Beverly S.
?
? TITLE: Effects of Human T Lymphocyte Activation on Inosine
?
? TITLE: Monophosphate Dehydrogenase Expression
?
? JOURNAL: J. Immunol.
?
?
? VOLUME: 152
?
? PAGES: 984-991
?
? DATE: 1994
?
?

```


US-09-853-918-20

Query Match 71.1%; Score 1862; DB 10; Length 384;
Best Local Similarity 73.9%; Pred. No. 5e-149;
Matches 380; Conservative 1; Mismatches 3; Indels 130; Gaps 1;

QY 1 MADYLISGTSYVDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
Db 1 MADYLISGTSYVDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
QY 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCNCTPEFOANEVRKVKYEOGFITDPVV 120
Db 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCNCTPEFOANEVRKVKYD----- 111
QY 121 LSPKDRVRDYFEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCLFLEEIMT 180
Db 112 ----- 111
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDELVAIARTDLKKNRDYPLASKDA 240
Db 112 ----- 111
QY 241 KKQLCGAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 300
Db 112 -KTLLCGAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 170
QY 301 GGNVNTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPOATAVYKVEYARRFGVP 360
Db 171 GGNVNTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPOATAVYKVEYARRFGVP 230
QY 361 VIADGQIONVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420
Db 231 VIADGQIONVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 290
QY 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVYPYLIAGIQHSCQDIDGAKSLTOVR 480
Db 291 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVYPYLIAGIQHSCQDIDGAKSLTOVR 350
QY 481 AMMSGELKFEKRTSSAQVEGVHSLHSYEKRLF 514
Db 351 AMMSGELKFEKRTSSAQVEGVHSLHSYEKRLF 384

RESULT 8

US-09-853-918-34
; Sequence 34, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; PRIOR APPLICATION NUMBER: 2001-05-10
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-34

Query Match 71.1%; Score 1861.5; DB 10; Length 385;
Best Local Similarity 74.3%; Pred. No. 5.5e-149;

Matches 382; Conservative 0; Mismatches 3; Indels 129; Gaps 2;

QY 1 MADYLISGTSYVDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
Db 1 MADYLISGTSYVDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
QY 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCNCTPEFOANEVRKVKYEOGFITDPVV 120
Db 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCNCTPEFOANEVRKVKY----- 110
QY 121 LSPKDRVRDYFEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCLFLEEIMT 180
Db 111 -SP----- 112
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDELVAIARTDLKKNRDYPLASKDA 240
Db 113 ----- 112
QY 241 KKQLCGAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 300
Db 113 -TQLCGAIGTHEDDKYRLDLLAQAGVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 171
QY 301 GGNVNTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPOATAVYKVEYARRFGVP 360
Db 172 GGNVNTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPOATAVYKVEYARRFGVP 231
QY 361 VIADGQIONVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420
Db 232 VIADGQIONVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 291
QY 421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVYPYLIAGIQHSCQDIDGAKSLTOVR 480
Db 292 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVYPYLIAGIQHSCQDIDGAKSLTOVR 351
QY 481 AMMSGELKFEKRTSSAQVEGVHSLHSYEKRLF 514
Db 352 AMMSGELKFEKRTSSAQVEGVHSLHSYEKRLF 385

RESULT 9

US-09-853-918-32
; Sequence 32, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; PRIOR APPLICATION NUMBER: 2001-05-10
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-32

Query Match 71.0%; Score 1860.5; DB 10; Length 385;
Best Local Similarity 74.1%; Pred. No. 6.7e-149;
Matches 381; Conservative 2; Mismatches 2; Indels 129; Gaps 2;

QY 1 MADYLISGTSYVDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
|||||

Db 1 MADYLISGGSYVPDDGLTAQQLFNCGGDLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLYSSPMDTVTEAGMAIAMALTGGIGFIHNCNTPPEFQANEVRKVKYEOGFITDPVV 120
Db 61 LKTPLYSSPMDTVTEAGMAIAMALTGGIGFIHNCNTPPEFQANEVRKVKYQ----- 111
QY 121 LSPKDRVDFEAKARHGFSGIPITDTGRMGSRVLGIISSRIDFLKKEEHDCLFEIIMT 180
Db 112 ----- 111
QY 181 KREDLVVAPRSITLKEANEILORSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db 112 -----PQS----- 114
QY 241 KKQLCGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKYYIKDKYPNLQVI 300
Db 115 ---LLCGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKYYIKDKYPNLQVI 171
QY 301 GGNVYTAQAQAKNLIDAGVDALRVGMSGSSICIIQEVLAGCRPQATAVYKVEYARFGVP 360
Db 172 GGNVYTAQAQAKNLIDAGVDALRVGMSGSSICITQEVLAGCRPQATAVYKVEYARFGVP 231
QY 361 VIADGGIQNVGHIKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 420
Db 232 VIADGGIQNVGHIKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 291
QY 421 DKHLSSQNRFFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480
Db 292 DKHLSSQNRFFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 351
QY 481 AMMSGELKFEKRTSSAQVEGVHSLHSEKRLF 514
Db 352 AMMSGELKFEKRTSSAQVEGVHSLHSEKRLF 385

RESULT 10
US-09-853-918-29
: Sequence 29, Application US/09853918
: Patent No. US20020068346A1
: GENERAL INFORMATION:
: APPLICANT: Krystek, Stanley R.
: APPLICANT: Sheriff, Steven
: APPLICANT: Witmer, Mark R.
: APPLICANT: Hollenbaugh, Diane L.
: APPLICANT: Yan, Ning
: APPLICANT: Mouravieff, Julie E.
: APPLICANT: Einspahr, Howard M.
: APPLICANT: Kish, Kevin
: TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
: FILE REFERENCE: DB24NP
: CURRENT APPLICATION NUMBER: US/09/853,918
: CURRENT FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: 60/203,448
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 29
: LENGTH: 384
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-853-918-29

Query Match 71.0%; Score 1860; DB 10; Length 384;
Best Local Similarity 73.9%; Pred. No. 7.4e-149;
Matches 380; Conservative 0; Mismatches 4; Indels 130; Gaps 1;

QY 1 MADYLISGGSYVPDDGLTAQQLFNCGGDLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
Db 1 MADYLISGGSYVPDDGLTAQQLFNCGGDLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLYSSPMDTVTEAGMAIAMALTGGIGFIHNCNTPPEFQANEVRKVKYEOGFITDPVV 120

Db 61 LKTPLYSSPMDTVTEAGMAIAMALTGGIGFIHNCNTPPEFQANEVRKVKYSG----- 113
QY 121 LSPKDRVDFEAKARHGFSGIPITDTGRMGSRVLGIISSRIDFLKKEEHDCLFEIIMT 180
Db 114 ----- 113
QY 181 KREDLVVAPRSITLKEANEILORSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db 114 ----- 113
QY 241 KKQLCGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKYYIKDKYPNLQVI 300
Db 114 ---LLCGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQINMIKYYIKDKYPNLQVI 170
QY 301 GGNVYTAQAQAKNLIDAGVDALRVGMSGSSICIIQEVLAGCRPQATAVYKVEYARFGVP 360
Db 171 GGNVYTAQAQAKNLIDAGVDALRVGMSGSSICITQEVLAGCRPQATAVYKVEYARFGVP 230
QY 361 VIADGGIQNVGHIKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 420
Db 231 VIADGGIQNVGHIKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 290
QY 421 DKHLSSQNRFFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480
Db 291 DKHLSSQNRFFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 350
QY 481 AMMSGELKFEKRTSSAQVEGVHSLHSEKRLF 514
Db 351 AMMSGELKFEKRTSSAQVEGVHSLHSEKRLF 384

RESULT 11
US-09-853-918-36
: Sequence 36, Application US/09853918
: Patent No. US20020068346A1
: GENERAL INFORMATION:
: APPLICANT: Krystek, Stanley R.
: APPLICANT: Sheriff, Steven
: APPLICANT: Witmer, Mark R.
: APPLICANT: Hollenbaugh, Diane L.
: APPLICANT: Yan, Ning
: APPLICANT: Mouravieff, Julie E.
: APPLICANT: Einspahr, Howard M.
: APPLICANT: Kish, Kevin
: TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
: FILE REFERENCE: DB24NP
: CURRENT APPLICATION NUMBER: US/09/853,918
: CURRENT FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: 60/203,448
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 36
: LENGTH: 385
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-853-918-36

Query Match 71.0%; Score 1859.5; DB 10; Length 385;
Best Local Similarity 73.9%; Pred. No. 8.2e-149;
Matches 380; Conservative 1; Mismatches 4; Indels 129; Gaps 1;

QY 1 MADYLISGGSYVPDDGLTAQQLFNCGGDLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
Db 1 MADYLISGGSYVPDDGLTAQQLFNCGGDLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLYSSPMDTVTEAGMAIAMALTGGIGFIHNCNTPPEFQANEVRKVKYEOGFITDPVV 120
Db 61 LKTPLYSSPMDTVTEAGMAIAMALTGGIGFIHNCNTPPEFQANEVRKVKY----- 110
QY 121 LSPKDRVDFEAKARHGFSGIPITDTGRMGSRVLGIISSRIDFLKKEEHDCLFEIIMT 180

Db 111 ----- 110
QY 181 KREDLVAPRSITLKEANEILÖRSKKGLPIVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db 111 ----- 111
QY 241 KKÖLLCGAAGTTHEDDKYRLDLLAÖAGVDVVLDDSSÖGNSIFÖJNMIRKIKDKYPNLÖVI 300
Db 112 GRPLLCGAAICTHEDDKYRLDLLAÖAGVDVVLDDSSÖGNSIFÖJNMIRKIKDKYPNLÖVI 171
QY 301 GGNVVTAAQAKNLLIDAGVDALRVGMGSGSICITÖEVLACGRPQATAYKVKVEYARREGVP 360
Db 172 GGNVVTAAQAKNLLIDAGVDALRVGMGSGSICITÖEVLACGRPQATAYKVKVEYARREGVP 231
QY 361 VIADGGIÖNVGHIKAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 420
Db 232 VIADGGIÖNVGHIKAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 291
QY 421 DKHLSSÖNRYFSEADKIKVAÖGVS GAVÖDKGSIHKFVPLYLAGIÖHSCÖDIGAKSLTÖVR 480
Db 292 DKHLSSÖNRYFSEADKIKVAÖGVS GAVÖDKGSIHKFVPLYLAGIÖHSCÖDIGAKSLTÖVR 351
QY 481 AMYSGELKFEKRTSSAÖVEGGVHSLHSTYEKRLE 514
Db 352 AMYSGELKFEKRTSSAÖVEGGVHSLHSTYEKRLE 385

RESULT 12
US-09-853-918-24
; Sequence 24, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-24

Query Match 70.9%; Score 1858; DB 10; Length 384;
Best Local Similarity 74.1%; Pred. No. 1.1e-148;
Matches 381; Conservative 1; Mismatches 2; Indels 130; Gaps 2;

QY 1 MADYLLISGTSYVPDDGLTAÖÖLFNCBGDLTYNDFLLILPGYIDFTADQYDLTSALTKKIT 60
Db 1 MADYLLISGTSYVPDDGLTAÖÖLFNCBGDLTYNDFLLILPGYIDFTADQYDLTSALTKKIT 60
QY 61 LKTPLVSSPMDTYTEAGMAIAMALTGGIGTTHNCTPEFQÖANEVRKVKYEQGFITDPV 120
Db 61 LKTPLVSSPMDTYTEAGMAIAMALTGGIGTTHNCTPEFQÖANEVRKVKYEQGFITDPV 111
QY 121 LSPKDRVDFEAKARHGFCGIPITDTGRMGSRVLVGISSRDIDFLKEEHDCFLIEIMT 180
Db 112 ----- 111
QY 181 KREDLVAPRSITLKEANEILÖRSKKGLPIVNEDELVAIIARTDLKKNRDYPLASKDA 240

Db 112 -----PI----- 113
QY 241 KKÖLLCGAAGTTHEDDKYRLDLLAÖAGVDVVLDDSSÖGNSIFÖJNMIRKIKDKYPNLÖVI 300
Db 114 --LLCGAAGTTHEDDKYRLDLLAÖAGVDVVLDDSSÖGNSIFÖJNMIRKIKDKYPNLÖVI 170
QY 301 GGNVVTAAQAKNLLIDAGVDALRVGMGSGSICITÖEVLACGRPQATAYKVKVEYARREGVP 360
Db 171 GGNVVTAAQAKNLLIDAGVDALRVGMGSGSICITÖEVLACGRPQATAYKVKVEYARREGVP 230
QY 361 VIADGGIÖNVGHIKAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 420
Db 231 VIADGGIÖNVGHIKAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAM 290
QY 421 DKHLSSÖNRYFSEADKIKVAÖGVS GAVÖDKGSIHKFVPLYLAGIÖHSCÖDIGAKSLTÖVR 480
Db 291 DKHLSSÖNRYFSEADKIKVAÖGVS GAVÖDKGSIHKFVPLYLAGIÖHSCÖDIGAKSLTÖVR 350
QY 481 AMYSGELKFEKRTSSAÖVEGGVHSLHSTYEKRLE 514
Db 351 AMYSGELKFEKRTSSAÖVEGGVHSLHSTYEKRLE 384

RESULT 13
US-09-853-918-37
; Sequence 37, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DE24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-37

Query Match 70.9%; Score 1857.5; DB 10; Length 385;
Best Local Similarity 74.1%; Pred. No. 1.2e-148;
Matches 381; Conservative 0; Mismatches 4; Indels 129; Gaps 2;

QY 1 MADYLLISGTSYVPDDGLTAÖÖLFNCBGDLTYNDFLLILPGYIDFTADQYDLTSALTKKIT 60
Db 1 MADYLLISGTSYVPDDGLTAÖÖLFNCBGDLTYNDFLLILPGYIDFTADQYDLTSALTKKIT 60
QY 61 LKTPLVSSPMDTYTEAGMAIAMALTGGIGTTHNCTPEFQÖANEVRKVKYEQGFITDPV 120
Db 61 LKTPLVSSPMDTYTEAGMAIAMALTGGIGTTHNCTPEFQÖANEVRKVKYEQGFITDPV 110
QY 121 LSPKDRVDFEAKARHGFCGIPITDTGRMGSRVLVGISSRDIDFLKEEHDCFLIEIMT 180
Db 111 ----- 110
QY 181 KREDLVAPRSITLKEANEILÖRSKKGLPIVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db 111 ----- 114
QY 241 KKÖLLCGAAGTTHEDDKYRLDLLAÖAGVDVVLDDSSÖGNSIFÖJNMIRKIKDKYPNLÖVI 300

Db 115 ---LLCGAIGTHEDDKYRLDLLAQAQVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 171

QY 301 GGNVYTAQAQAKNLIDAGVDALRVGMGSGSICITQEVVLACGRPQATAVYKVSEYARREGVP 360

Db 172 GGNVYTAQAQAKNLIDAGVDALRVGMGSGSICITQEVVLACGRPQATAVYKVSEYARREGVP 231

QY 361 VIADGCIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420

Db 232 VIADGCIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 291

QY 421 DKHLSSQNRIFYSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480

Db 292 DKHLSSQNRIFYSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 351

QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514

Db 352 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 385

RESULT 14

US-09-853-918-38

; Sequence 38, Application US/09853918

; Patent No. US20020068346A1

; GENERAL INFORMATION:

; APPLICANT: Krystek, Stanley R.

; APPLICANT: Sheriff, Steven

; APPLICANT: Wilmer, Mark R.

; APPLICANT: Hollenbaugh, Diane L.

; APPLICANT: Yan, Ning

; APPLICANT: Mouravieff, Julie E.

; APPLICANT: Einspahr, Howard M.

; APPLICANT: Kish, Kevin

; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE

; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF

; FILE REFERENCE: DB24NP

; CURRENT APPLICATION NUMBER: US/09/853,918

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 60/203,448

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 38

; LENGTH: 385

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-853-918-38

Query Match 70.9%; Score 1857.5; DB 10; length 385;

Best Local Similarity 74.1%; Pred. No. 1.2e-148;

Matches 381; Conservative 0; Mismatches 4; Indels 129; Gaps 2;

QY 1 MADYLISGTSYVPDDGLTAAQLFNCGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60

Db 1 MADYLISGTSYVPDDGLTAAQLFNCGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60

QY 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCTPEFQANEVRKVKYKYEQGFTDPVV 120

Db 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCTPEFQANEVRKVKYKYS----- 112

QY 121 LSPKDRVRFVEAKARHGFCGIPITDTGRMGSRVLGIISSRIDIDFLKEEHDCFLLEIMT 180

Db 113 ----- 112

QY 181 KREDLVVAPRSTITLKEANEILQRSKKGKLPIVNEDELVAIIARTDLKKNRDYPLASKDA 240

Db 113 -----PL----- 114

QY 241 KKQLLCGAIGTHEDDKYRLDLLAQAQVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 300

Db 115 ---LLCGAIGTHEDDKYRLDLLAQAQVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 171

QY 301 GGNVYTAQAQAKNLIDAGVDALRVGMGSGSICITQEVVLACGRPQATAVYKVSEYARREGVP 360

Db 172 GGNVYTAQAQAKNLIDAGVDALRVGMGSGSICITQEVVLACGRPQATAVYKVSEYARREGVP 231

QY 361 VIADGCIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420

Db 232 VIADGCIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 291

QY 421 DKHLSSQNRIFYSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 480

Db 292 DKHLSSQNRIFYSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVR 351

QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514

Db 352 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 385

RESULT 15

US-09-853-918-22

; Sequence 22, Application US/09853918

; Patent No. US20020068346A1

; GENERAL INFORMATION:

; APPLICANT: Krystek, Stanley R.

; APPLICANT: Sheriff, Steven

; APPLICANT: Wilmer, Mark R.

; APPLICANT: Hollenbaugh, Diane L.

; APPLICANT: Yan, Ning

; APPLICANT: Mouravieff, Julie E.

; APPLICANT: Einspahr, Howard M.

; APPLICANT: Kish, Kevin

; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE

; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF

; FILE REFERENCE: DB24NP

; CURRENT APPLICATION NUMBER: US/09/853,918

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 60/203,448

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 22

; LENGTH: 384

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-853-918-22

Query Match 70.9%; Score 1857; DB 10; length 384;

Best Local Similarity 74.1%; Pred. No. 1.3e-148;

Matches 381; Conservative 0; Mismatches 3; Indels 130; Gaps 2;

QY 1 MADYLISGTSYVPDDGLTAAQLFNCGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60

Db 1 MADYLISGTSYVPDDGLTAAQLFNCGDLTYNDFLILPGYIDFTADQVDLTSLTKKIT 60

QY 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCTPEFQANEVRKVKYKYEQGFTDPVV 120

Db 61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHNCTPEFQANEVRKVKY----- 110

QY 121 LSPKDRVRFVEAKARHGFCGIPITDTGRMGSRVLGIISSRIDIDFLKEEHDCFLLEIMT 180

Db 111 -SP----- 112

QY 181 KREDLVVAPRSTITLKEANEILQRSKKGKLPIVNEDELVAIIARTDLKKNRDYPLASKDA 240

Db 113 ----- 112

QY 241 KKQLLCGAIGTHEDDKYRLDLLAQAQVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 300

Db 113 ---SLCGAIGTHEDDKYRLDLLAQAQVDVVLDDSSQGSNIFQINMIKIKDKYPNLQVI 170

QY 301 GGNVYTAQAQAKNLIDAGVDALRVGMGSGSICITQEVVLACGRPQATAVYKVSEYARREGVP 360

Db 171 GGNVYTAQAQAKNLIDAGVDALRVGMGSGSICITQEVVLACGRPQATAVYKVSEYARREGVP 230

QY 361 VIADGCIQNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420

Db	231	VIADGGIONVGHIAKALALGASTVMGSLLAATTEAPGEYFFSDGIRLTKYRGMGLDAM	290
QY	421	DKHLSSQNRRYFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIOHSCDDIGAKSLTQVR	480
Db	291	DKHLSSQNRRYFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIOHSCDDIGAKSLTQVR	350
QY	481	AMMYSGELKFEKRTSSAQVEGVHSLHSEKRLF	514
Db	351	AMMYSGELKFEKRTSSAQVEGVHSLHSEKRLF	384

Search completed: February 13, 2003, 11:17:22
Job time : 306 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 03:27:06 ; Search time 98 Seconds
(without alignments)
1080.696 Million cell updates/sec

Title: US-09-846-637C-4
Perfect score: 2619
Sequence: 1 MADYLISGTSYVPPDDGLTA.....SSAQVEGVHSLHSYEKRLF 514

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2561	97.8	514	11 Q91Z11	Q91Z11 mus muscula
2	2182	83.3	445	11 Q9DC16	Q9DC16 mus muscula
3	2079.5	79.4	489	4 Q96NU2	Q96NU2 homo sapien
4	1597.5	61.0	521	3 Q9P8J2	Q9P8J2 candida alb
5	1563	59.7	529	3 Q9UVL0	Q9UVL0 pneumocysti
6	1553.5	59.3	446	5 Q8SXM5	Q8SXM5 drosophila
7	1416	54.1	534	5 Q9GZH3	Q9GZH3 caenorhabdi
8	1173.5	44.8	510	5 Q96387	Q96387 plasmodium
9	1148	43.8	502	10 Q9ZPA0	Q9ZPA0 glycine max
10	1117	42.6	501	10 Q9AY75	Q9AY75 oryza sativ
11	973	37.2	484	16 Q8RC64	Q8RC64 thermocanaer
12	966.5	36.9	485	16 Q9PNN3	Q9PNN3 campylobact
13	958	36.6	485	16 Q97FM8	Q97FM8 clostridium
14	941.5	35.9	487	16 Q8XZG6	Q8XZG6 ralstonia s
15	922	35.2	485	16 Q9KGN8	Q9KGN8 bacillus ha
16	914	34.9	487	16 Q9JUD0	Q9JUD0 neisseria m

17	911	34.6	487	16 Q9JZB5	Q9JZB5 neisseria m
18	910.5	34.6	484	16 Q8X145	Q8X145 clostridium
19	910	34.7	485	16 Q9PAR5	Q9PAR5 xylella fas
20	904.5	34.5	482	16 Q9X168	Q9X168 thermotoga
21	901	34.4	487	16 Q8RE86	Q8RE86 fusobacteri
22	885	33.6	509	2 Q9RHG9	Q9RHG9 bacillus ce
23	878.5	33.5	509	2 Q9RHG1	Q9RHG1 bacillus ce
24	875	33.4	489	16 Q9HXM5	Q9HXM5 pseudomonas
25	860	32.6	488	16 Q99W19	Q99W19 staphylococ
26	858.5	32.6	499	16 Q8YBK4	Q8YBK4 brucella me
27	855.5	32.7	500	16 Q9RT87	Q9RT87 deinococcus
28	848	32.4	392	10 Q944T1	Q944T1 glycine max
29	846.5	32.3	488	16 Q926Y9	Q926Y9 listeria mo
30	846	32.3	489	16 Q9KRW3	Q9KRW3 vibrio chol
31	836	31.9	500	16 Q92RT5	Q92RT5 rhizobium m
32	832.5	31.6	493	16 Q9C1Y6	Q9C1Y6 lactococcus
33	827	31.6	487	16 Q8ZCU3	Q8ZCU3 yersinia pe
34	825.5	31.5	506	2 Q9RHZ0	Q9RHZ0 corynebacte
35	819.5	31.3	487	16 Q9A7V2	Q9A7V2 caulobacter
36	818	31.2	490	16 Q8Z4Q2	Q8Z4Q2 salmonella
37	818	31.2	503	16 Q8UHQ6	Q8UHQ6 agrobacteri
38	815.5	31.1	501	16 Q9L017	Q9L017 streptomyce
39	812.5	31.0	492	16 Q97NA3	Q97NA3 streptococ
40	807.5	30.6	500	16 Q983F6	Q983F6 rhizobium 1
41	793	30.3	500	16 Q978L4	Q978L4 thermoplasm
42	774.5	29.6	485	17 Q9HLK8	Q9HLK8 thermoplasm
43	747.5	28.5	485	17 Q8TV01	Q8TV01 methanopyru
44	746	28.5	502	17 Q8TV01	Q8TV01 methanopyru
45	737.5	28.2	484	17 Q26245	Q26245 methanobact

ALIGNMENTS

RESULT 1	Q91Z11	PRELIMINARY;	PRT;	514 AA.
ID	Q91Z11			
AC	Q91Z11;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Inosine 5'-phosphate dehydrogenase 2.			
GN	IMPDH2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC010314; AAH10314.1; -.			
DR	MGI; MGI:109367; Impdh2.			
DR	InterPro; IPR000644; CBS_domain.			
DR	InterPro; IPR003009; FMN_enzyme.			
DR	InterPro; IPR001093; IMPdh/GMPPrase.			
DR	Pfam; PF00571; CBS_2.			
DR	Pfam; PF00478; IMPDH_C; 1.			
DR	Pfam; PF01574; IMPDH_N; 1.			
DR	TIGRFAMS; TIGR01302; IMP_dehydrog; 1.			
DR	PROSITE; PS00487; IMP_DH_GMP_RED; UNKNOWN_1.			
SQ	SEQUENCE 514 AA; 55815 MW; 17D25A5C5EBCC439 CRC64;			

Query Match 97.8%; Score 2561; DB 11; Length 514;
Best local Similarity 98.1%; Pred. No. 2.1e-170;
Matches 504; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY	1	MADYLISGTSYVPPDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSA	TKKIT 60
DB	1	MADYLISGTSYVPPDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSA	TKKIT 60
OY	61	LKTPLVSSPMDITVTEAGMAIAMALTGGTGFHNCCTPEQANEVKRVKKYEQGFITDPV	120

Db 61 LKTPLVSSPMDVTVEAGMAIAMALTGIGIFIHNNCTPEFQANEVRKVKYEQGFITDPVV 120
QY 121 LSPKDRVDFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDFLEEIMT 180
Db 121 LSPKDRVDFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDFLEEIMT 180
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDELVAIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVVAPAGVTLKEANEILQRSKKGKLPIVNEDELVAIARTDLKKNRDYPLASKDA 240
QY 241 KKQLCGAIGTHEDDKYRLDLAQAQVDVVLDSQGSNIFQINMIKVIKDKYPNLQVI 300
Db 241 KKQLCGAIGTHEDDKYRLDLAQAQVDVVLDSQGSNIFQINMIKVIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMSGSSICITQEVLAGCRPQATAVYKVEYARRGVP 360
Db 301 GGNVVTAAQAKNLIDAGVDALRVGMSGSSICITQEVLAGCRPQATAVYKVEYARRGVP 360
QY 361 VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRXFSEADKIKVAQGVSGAVQDKGSIHKFPYLIAGIQHSCQDIGAKSLTQVR 480
Db 421 DKHLSSQNRXFSEADKIKVAQGVSGAVQDKGSIHKFPYLIAGIQHSCQDIGAKSLTQVR 480
QY 481 AMMYSGELEKFEKRTSSAQVEGCVHSLHSEYKRLF 514
Db 481 AMMYSGELEKFEKRTSSAQVEGCVHSLHSEYKRLF 514

RESULT 2

Q9DCL6 PRELIMINARY; PRT; 445 AA.

AC Q9DCL6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Inosine 5'-phosphate dehydrogenase 2.
GN IMPDH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK002676; BAB22278.1; -.
DR HSSP; P12268; 1B3O.
DR MGD; MGI:109367; Impdh2.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.

DR InterPro; IPR001093; IMPdh/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMs; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 445 AA; 48474 MW; 1B3A4006640CB4C9 CRC64;
Query Match 83.3%; Score 2182; DB 11; Length 445;
Best local Similarity 96.9%; Pred. No. 4.7e-144;
Matches 431; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 70 MDVTVEAGMAIAMALTGIGIFIHNNCTPEFQANEVRKVKYEQGFITDPVLSPKDRVVD 129
Db 1 MDVTVEAGMAIAMALTGIGIFIHNNCTPEFQANEVRKVKYEQGFITDPVLSPKDRVVD 60
QY 130 VFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDFLEEIMTKREDLVAP 189
Db 61 VFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDFLEEIMTKREDLVAP 120
QY 190 RSITLKEANEILQRSKKGKLPIVNEDELVAIARTDLKKNRDYPLASKDAKKQLCGAA 249
Db 121 AGVTLKEANEILQRSKKGKLPIVNEDELVAIARTDLKKNRDYPLASKDAKKQLCGAD 180
QY 250 IGTTHEDDKYRLDLAQAQVDVVLDSQGSNIFQINMIKVIKDKYPNLQVIGNVVTTAAQ 309
Db 181 IGTTHEDDKYRLDLAQAQVDVVLDSQGSNIFQINMIKVIKDKYPNLQVIGNVVTTAAQ 240
QY 310 AKNLIDAGVDALRVGMSGSSICITQEVLAGCRPQATAVYKVEYARRGVPVIADGQIN 369
Db 241 AKNLIDAGVDALRVGMSGSSICITQEVLAGCRPQATAVYKVEYARRGVPVIADGQIN 300
QY 370 VGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAMDHLSSQNR 429
Db 301 VGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAMDHLSSQNR 360
QY 430 YFSEADKIKVAQGVSGAVQDKGSIHKFPYLIAGIQHSCQDIGAKSLTQVRAMYSGELE 489
Db 361 YFSEADKIKVAQGVSGAVQDKGSIHKFPYLIAGIQHSCQDIGAKSLTQVRAMYSGELE 420
QY 490 FEKRTSSAQVEGCVHSLHSEYKRLF 514
Db 421 FEKRTSSAQVEGCVHSLHSEYKRLF 445

RESULT 3

Q96NU2 PRELIMINARY; PRT; 489 AA.

AC Q96NU2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA FLJ30078 fis, clone BGG112000533, highly similar to
DE inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK054640; BAB70780.1; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001295; DHO_dh.

DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPdh/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00912; DHODEHASE_2; UNKNOWN_1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; UNKNOWN_1.
SQ SEQUENCE 489 AA; 52597 MW; 47A1273662A8C39B CRC64

Query Match 79.4%; Score 2079.5; DB 4; Length 489;
Best Local Similarity 78.8%; Pred. No. 7.7e-137;
Matches 405; Conservative 39; Mismatches 45; Indels 25; Gaps 1;

QY 1 MADYLLISGTSYVPDDGLTAOQLFNCGDGLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
DB 1 MADYLLISGTSYVPDDGLTAOQLFNCGDGLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMALTGIGTIIHNCTPEFOANEVRKVKYEOGFTTDPVV 120
DB 61 LKTPLVSSPMDVTVEAGMAIAMALTGIGTIIHNCTPEFOANEVRKVKYEOGFTTDPVV 120
QY 121 LSPKDRVRDVEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCFLLEIMT 180
DB 96 LSPSHTVGDVLEAKMRHGFSGIPITETGTMGSKLVGIVTSRDIDFLAKDHTTLLSEVMT 155
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
DB 156 PRIELVVAPAGVTLKEANEILQRSKKGKLPVNDCELVAIIARTDLKKNRDYPLASKDS 215
QY 241 KQQLCGAATGTHEDDKYRLDLAAGVDVNVLLDSSOGNSIFQINMIRYIKDKYPNLOVI 300
DB 216 QKQLCGAAGTREDDKYRLDLTAQADVIVLDSOGNSVQIAMVYIKQYPHLOVI 275
QY 301 GGNVNTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGRPOATAVYKVEYARFGVP 360
DB 276 GGNVNTAAQAKNLIDAGVDGLRVGMGSGSICITQEVMACGRPOGTAVYKVAEYARFGVP 335
QY 361 VIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRKKYRGMSLDAM 420
DB 336 IADGGIQTGVHVKALALGASTVMGSLAATTEAPGEYFFSDGIRKKYRGMSLDAM 395
QY 421 DKHLSSQNRYSFSEADKIKVAQGVSGAVODKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480
DB 396 EKSSSSQKRYFSEGDVKVIAQGVSGSIDKGSIOKFVPYLIAGIQHSCQDIGARSLVLR 455
QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSEKRL 514
DB 456 SMMYSGELKFEKRTMSAOIEGVHGLHSEKRL 489

RESULT 4

Q9P8J2 PRELIMINARY; PRT; 521 AA.
AC Q9P8J2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative inosine 5'-monophosphate dehydrogenase.
GN IMH3.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1006;
RX MEDLINE=20569171; PubMed=11119495;
RA Beckerman J., Chibana H., Turner J., Magee P.T.;
RT "Single-copy IMH3 allele is sufficient to confer resistance to
mycophenolic acid in Candida albicans and to mediate transformation of
clinical Candida species.";
RL Infect. Immun. 69:108-114(2001).

DR EMBL; AF249293; AAF70813.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPdh/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
FT VARIANT 47 47 V -> I.
FT VARIANT 102 102 A -> S.
FT VARIANT 400 400 D -> G.
SQ SEQUENCE 521 AA; 56267 MW; 7A1CF4DF6184FE7E CRC64;

Query Match 61.0%; Score 1597.5; DB 3; Length 521;
Best Local Similarity 63.1%; Pred. No. 3.6e-103;
Matches 327; Conservative 69; Mismatches 107; Indels 15; Gaps 6;

QY 7 SGGTSYVPD---DGLTAOQLFNCGD--GLTYNDFLLPGYIDFTADQVDTLSALTKKIT 60
DB 6 SKATSYLKDYRKKGKDLGVKELIDSTNFGGLTYNDFLLPGLVNFPSSAVSLETCLKTKIT 65
QY 61 LKTPLVSSPMDVTVEAGMAIAMALTGIGTIIHNCTPEFOANEVRKVKYEOGFTTDPVV 120
DB 66 LKSPFVSSPMDVTVEENMAIHMAALLGIGTIIHNCTAEQAEVWRKVKYENGFINDPVV 125
QY 121 LSPKDRVRDVEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCFLLEIMT 180
DB 126 ISPEVTGEVYKMGVEVLGFTSFPTENGKVGKLVGIITSRDIOF--HEDNKSPVSEVMT 183
QY 181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKD- 239
DB 184 K-DLVVGKKGISLTDGNELLRSSKKGKLPVDAEGLVSLISRTDLQKNQDYPNASKSF 241
QY 240 AKKQLCGAATGTHEDDKYRLDLAAGVDVNVLLDSSOGNSIFQINMIRYIKDKYPNLOV 299
DB 242 HSKQLCGAATGTHEDDKYRLDLAAGVDVNVLLDSSOGNSVFOINMIRYIKDKYPNLOV 301
QY 300 IAGNVVTRDQALVLEAGADALRVGMGSGSICITQEVMACGRPOGTAVYKVEYARFGV 359
DB 302 IAGNVVTRDQALVLEAGADALRVGMGSGSICITQEVMACGRPOGTAVYKVEYARFGV 361
QY 360 PVIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDA 419
DB 362 PCIADGGIONVGHITKALALGASCVMGGLLAGTAETPDYFYRQGRKRLKTYRGMSIDA 421
QY 420 MDKHLSSQN---RYFSEADKIKVAQGVSGAVODKGSIHKFVPYLIAGIQHSCQDIGAKS 475
DB 422 MQQTNTNANASTSRYSFSEADKVLVAQGVSGSVVDKGSITKFVPYLYNGLQHSLODIGIKS 481
QY 476 LTQVRAMYSGELKFEKRTSSAQVEGCVHSLHSEKRL 513
DB 482 IDELRENVNDGEIRFEFRTASAOIFEGCVHGLHSEKRL 519

RESULT 5

Q9UVL0 PRELIMINARY; PRT; 529 AA.
AC Q9UVL0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Pneumocystis carinii.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125226; PubMed=11223253;
RA Ye D., Lee C.H., Queener S.F.;

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RT "Differential splicing of Pneumocystis carinii f. sp. carinii inosine
RL 5'-monophosphate dehydrogenase pre-mRNA."
RL Gene 263:151-158(2001).
DR EMBL; AF196975; AAF13230.1; -.
DR HSSP; P12268; 1B3O.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPdh/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 529 AA; 58066 MW; 030573A8854ADB5A CRC64;

Query Match 59.7%; Score 1563; DB 3; Length 529;
Best Local Similarity 61.4%; Pred. No. 9.5e-101;
Matches 316; Conservative 69; Mismatches 112; Indels 18; Gaps 7;

QY 12 YVPDDGLTAQQLFNGC--DGLTYNDFLLPGYIDFTADQVDLTSLTKTKTLPLVSS 68
   || || || || || || || || || || || || || || || || || || || ||
Db 20 YSEKDGIDLDLI-CSRRHGGLTYNDIILPGYIDFEVNSVLSLHSHITKKIVLKTPEMSS 78

QY 69 PMDTVEAGMAIAMALTGGIGFIHNCTPEFQANEVRKVKKYEQGFITDPVLSPKDRVR 128
   || || || || || || || || || || || || || || || || || || || ||
Db 79 PMDTVESDMAINLALLGGIGVIHNCTIEQTEMVNRKVKKFENGFITSPIVLSLNHVR 138

QY 129 DVEAKARHGFCCGIPITDTGRMGSRVGISSRDIDFLKEEHDCFLLEIMTKREDLVVA 188
   || || || || || || || || || || || || || || || || || || || ||
Db 139 DVRRIKEELFGSGIPITDTGLNGKLGIIVTSRDIQFHNNDE--SLSEVMTK--DLVTG 194

QY 189 PRSITLKEANEILQRSKKGKLPIVNEDELVAIIARTDLKKNRDYPLASK-DAKKQLCG 247
   || || || || || || || || || || || || || || || || || || || ||
Db 195 SEGIRLEEANEILRSCKKGLPIVDKGNLTALLSRSDLMKNLHFLASKLPDSKQLICA 254

QY 248 AALGTHEDDKYRLDLLAQAGVDVVVLDSQGSIFQINMIKIKDKYPNLQVIGNVTA 307
   || || || || || || || || || || || || || || || || || || || ||
Db 255 AAVGTRPDDRIRLKLHVEAGLDIVLDSQGSNIYQINMIKIKKEFPNLEVIAGNVTR 314

QY 308 AQAKNLIDAGVDALRVGMSGSGICITQEVLAGCRPQATAVYKYVEYARRFVPIADGCI 367
   || || || || || || || || || || || || || || || || || || || ||
Db 315 EQAANLISAGADALRVGMSGSGICITQEI MAVGRPQATAVYAVSEFASKFGVPTIADGCI 374

QY 368 QNVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAMDKHLSQ 427
   || || || || || || || || || || || || || || || || || || || ||
Db 375 ENGHITKALALGASAVMMGNLLAGTTESPGQYYR DGQRLKSYRGMSIDAME-HLSGK 433

QY 428 N-----RYFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQV 479
   || || || || || || || || || || || || || || || || || || || ||
Db 434 NKGDNASSRYFGEADTIRVAQGVSGSVIDKGLHVVYPYLRTGLQHSLODIGVQNLTEL 493

QY 480 RAMMYSGELKFEKRTSSAOVEGVSLSHYEKRLE 514
   | : || || || || || || || || || || || || || || || || || || ||
Db 494 RKQVKEKNIRFEERTVASQLGQNVHGLDSYQKKLW 528

RESULT 6
Q8SXM5 PRELIMINARY; PRT; 446 AA.
AC Q8SXM5;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE LD36080p.
GN RAS.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guartín H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY089553; AAL90291.1; -.
SQ SEQUENCE 446 AA; 48139 MW; 15746E0A799702BB CRC64;

Query Match 59.3%; Score 1553.5; DB 5; Length 446;
Best Local Similarity 67.5%; Pred. No. 3.4e-100;
Matches 303; Conservative 63; Mismatches 76; Indels 7; Gaps 3;

QY 70 MDVTVEAGMAIAMALTGGIGFIHNCTPEFQANEVRKVKKYEQGFITDPVLSPKDRYRD 129
   || || || || || || || || || || || || || || || || || || || ||
Db 1 MDVTVESEMAIAMALCGGIGFIHNCTPEYQALEVHKVKYKHGMRDPSVMSPTNTVGD 60

QY 130 VFEAKARHGFCCGIPITDTGRMGSRVGISSRDIDFLKEEHDCFLLEIMTKREDLVVA 189
   || || : || || || || || || || || || || || || || || || || || ||
Db 61 VLEARRKNGFTGYPVTENGKLGKLLGMVTSRDIDF-RENQPEVLLADIMT--TELVYAP 117

QY 190 RSITLKEANEILQRSKKGKLPIVNEDELVAIIARTDLKKNRDYPLASKDAKKQLLCGAA 249
   || || || || || || || || || || || || || || || || || || || ||
Db 118 NGINLPTANAILEKSKKGLPIVNOAGELVAMIARTDLKARSYPNASKDSNKQLVGA 177

QY 250 IGTTHEDDKYRLDLLAQAGVDVVVLDSQGSIFQINMIKIKDKYPNLQVIGNVTAQ 309
   || || || || || || || || || || || || || || || || || || || ||
Db 178 IGTRESEDKARLALLVANGVDVILDSQGSNSVYQVEMIKYIKETYPQLQVIGNVTRAQ 237

QY 310 AKNLIDAGVDALRVGMSGSGICITQEVLAGCRPQATAVYKYVEYARRFVPIADGCIQ 369
   || || || || || || || || || || || || || || || || || || || ||
Db 238 AKNLIDAGVDGLRVGMSGSGICITQEVMAACGCPQATAVYQYSTYARQFGVPIADGCIQS 297

QY 370 VGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAMD---KHL 425
   || || || || || || || || || || || || || || || || || || || ||
Db 298 IGHIVKALALGASAVMMGSLAGTSEAPGEYFFSDGVRLKKYRGMSLEAMERDAKGA 357

QY 426 SQNRYFSEADKIKVAQVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVRAMYS 485
   | : || || || || || || || || || || || || || || || || || || ||
Db 358 MSRYVHNEMDKMKVAQGVSGSLVDKGSVLRYPYLECGLQHSQDIGANSINKLRDMYN 417

QY 486 GELKFEKRTSSAOVEGVSLSHYEKRLE 514
   || || || || || || || || || || || || || || || || || || || ||
Db 418 GQLRFMKRTHSAQLEGVNHGLFSYEKRLE 446

RESULT 7
Q9GZH3 PRELIMINARY; PRT; 534 AA.
AC Q9GZH3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 58.2 kDa protein.
GN T22D1.3.
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; Pubmed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Geisel C., Bradshaw H., Hawkins M.;
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RT "The sequence of C. elegans cosmid T22D1.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039052; AAF98635.2; -.
DR HSSP; P12268; 1B3O.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR01093; IMPDh/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Hypothetical protein.
SQ SEQUENCE 534 AA; 58170 MW; 9462FBEE9119FD0B CRC64;

Query Match 54.1%; Score 1416; DB 5; Length 534;
Best Local Similarity 53.9%; Pred. No. 1.8e-90;
Matches 281; Conservative 98; Mismatches 116; Indels 26; Gaps 7;

QY 16 DGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSAITKTKITLPLVSSPMDVTVE 75
DB 18 DGETVHEMMAHKAAGLTYNDFNLPGLFNGVHDVSLSTNITKDKIKPLVSSPMDVTVE 77
QY 76 AGMAIAMALTGIGTGFTHHNC-TPEFOANEVRRKYKYEQGFTDPVVLSPKDRVRDVEAK 134
DB 78 SGMAIVMALYGGIGTIGHNFPKPEDQAAEVLKYKRFKQGYVMQPHCLSRDSTAFDMIQIK 137
QY 135 ARHGFSGIPITDTGRMGSRVLVGISSRDIDFLK-----EEEHDCF-----LEEIM 179
DB 138 KKYGTGAPVTEGDRGVSKLIGMVTSRDFEITMDVAGQKGTPISDTNDVYPTPTPTTRIM 197
QY 180 TKREDLVVAPRSTILKEANELLQSRKK---GKLPIVNEDELVAIIRPTDLKKNRDYPL 235
DB 198 VSVDOQLHLG----HINDAPELSQKKLKEHRLGKLPIVNDNGELCALLGRSLLKARDYPM 253
QY 236 ASKDAKKQLLCGAAGCTHEDDKYRLDLLAQAGVDVVLDSQGSNIFETINMIKIKDKYP 295
DB 254 ASYDSKGQLLCGAAVNTRGESQYTVDRVEAGVDVLLIDSSNGSSTYQISMRLYIKEKHP 313
QY 296 NLQVIGGNVNTAAQAKNLIDAGVDALRVGMSGISICIIQEVLAGCRPAATAVYKVEYAR 355
DB 314 HVQVIAGNVTRAQAKLLIDGADGLRIGMSGISICITQDVMAVGRACTAVYDVARYAN 373
QY 356 RFGVPVIADGQIONVGHIAKALALGASTVMGSLAATTEAPGEYFES--DCIRLKYYRGM 414
DB 374 QRGIPIVADGQIRDVGYITKAISLGASAVVMGGLLAATTEAPGEYFEGEDGCVRVKKYRGM 433
QY 415 GSLDAMDKHLSSQNRVF-SEADKIKVAQGVSGAVQDKGSIHKFVPIYLAGIQHSCQDIGA 473
DB 434 GSLDAMEAHASSQDRYFTAESDQIKVAQGVSATMKGDSCHKFIPIYLRGVQHGMDIGV 493
QY 474 KSLTQVRAMMYSGELKFEKRTSSAQVEGVSHLSYEKRLF 514
DB 494 RSLRDFREKVDNGIVKFERRSTNAQLECGVSHLSFEKRLY 534

RESULT 8
O96387 PRELIMINARY; PRT: 510 AA.
AC O96387;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;

RN [1]
RP SEQUENCE FROM N.A.
RA Prosis G.L., James A.A., Luecke H.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035679; AAD10256.1; -.
DR HSSP; P12268; 1B3O.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR01093; IMPDh/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 510 AA; 56148 MW; 449413AD3E41A7D0 CRC64;

Query Match 44.8%; Score 1173.5; DB 5; Length 510;
Best Local Similarity 48.2%; Pred. No. 1.4e-73;
Matches 240; Conservative 96; Mismatches 147; Indels 15; Gaps 4;

QY 17 GLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSAITKTKITLPLVSSPMDVTVEA 76
DB 4 GWKADEVFGVMSYTYDVIICMPGYIDFALSDIDLNTNMTDNTLTKPTVYISSPMDVTGCH 63
QY 77 GMAIAMALTGIGTGFTHHNC-TPEFOANEVRRKYKYEQGFTDPVVLSPKDRVRDVEAKAR 136
DB 64 KMSIALALSGGLGYIHNMSIEKQIEEVKKYKRFENGFIIDPYTFSPETHVADVLETNR 123
QY 137 HGFCGIPITDTGRMGSRVLVGISSRDIDFLKEEHHDCFLEEIMTKREDLVVAPRSTILKE 196
DB 124 VGKSYPTITVDGKGVSKLVGIITG--IDYLVLTNKSMTKIGDIT--TDVVTGSYPINLSD 179
QY 197 ANEILQSRKKKGLPIVNEDELVAIARTDLKKNRDYPLASKDAKKQLLCGAAGCTHEDD 256
DB 180 ANKVLCEKKSVLPVKNKNELIALVCRNDMHKNRIFPHASKSQNKQLIVGASISTREHD 239
QY 257 KYRLDLLAQAGVDVVLDSQGSNIFQINMIKIKDKYPNLQVIGGNVNTAAQAKNLIDA 316
DB 240 LERANQLIKNMIDVICIDSSQGSNISTYQIDITIKIKSAHPDIPILIGGNVTSQAKNLIDA 299
QY 317 GVDALRVGMSGISICIIQEVLAGCRPAQATAVYKVEYARRFVPIADGQIONVGHIAKA 376
DB 300 GADVLRIGMSGISICTTQDVCAVGRAQGTAVYHVSRYAHTRNKTIADGQIKNSGNIVKA 359
QY 377 LALGASTVMGSLAATTEAPGEYFESDGIPLKYYRGMGLDAM-DKHLSSQNRVF---- 431
DB 360 LSLGADFVMLGNLDAATEESCESEYFENNVRLLKYYRGMGMEAMYNKGFNSKSRYLVDER 419
QY 432 -----SEADKIKVAQGVSGAVQDKGSIHKFVPIYLAGIQHSCQDIGASLTQVRAMYS 485
DB 420 KNEYTDENIDEIKVSQGVASLVDKGSVNLPIHLFKAVKHGFQSMGTRNIPELHSLYS 479
QY 486 GELKFEKRTSSAQVEGV 503
DB 480 GDIFRDVRSFNTIKEGV 497

RESULT 9
O9ZPAO PRELIMINARY; PRT: 502 AA.
AC O9ZPAO;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inosine monophosphate dehydrogenase.
GN IMPDH1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847; [1]

RP SEQUENCE FROM N.A.
RA Cao Y., Schubert K.R.;
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010201; CAB38030.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR01093; IMPdh/GMPrtase.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 502 AA; 53407 MW; 617AB87613C36AA4 CRC64;

Query Match 43.8%; Score 1148; DB 10; Length 502;
Best Local Similarity 48.8%; Pred. No. 8e-72;
Matches 247; Conservative 78; Mismatches 163; Indels 18; Gaps 7;

QY 15 DDGLTAQQLFNCGDGLTYNDLFLIPGYIDFTADQVDLTSAITKTKITLTPLVSSPMDTVT 74
Db 9 EDGFTAEEKLFYQCFSTYTYDDVIFLPHYIDFAADAVDLSTRLTRLLPLAVPVASPMDTV 68
QY 75 EAGMAIAMALTGGIGFIHNCPTPEFOANEVRKVKYEQGFITDPVVLSPKDRV--DVEE 132
Db 69 ESAMAAAMASLGGIAVVSHPAAYQAAILRRAKSRVPILSDPAFAAPSAVVEHDAFG 128
QY 133 AKARHGFSGIPITDTGRMGSRVLGIISSRIDFLKEEHDCLFLEIMTKREDLVAPRSI 192
Db 129 ASP----FLVYDTGTGSVGLGVARS--DWTNQTDKGLRVGDYMAPPK--PAPWNA 179
QY 193 TLKEANEILORSKKGLPIVNEDELVAIARTDLKKNRDYPL---ASKDAKKQLLGA 248
Db 180 DLNKINEIMESKSGAVAL-ERDEGVVDIVREEVERRGYPKLVAAPATVGADGEFMVGA 238
QY 249 AIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQIMIKYIKDKYPNLQYIGNVVTA 308
Db 239 AVGTREDDKERLEHLVKAGLNVVLDSQGSNIYQLEMVNVYKRVPELDVIGNVVTMY 298
QY 309 QAKNLIDAGVDALRVGMGSGSICIIOEVLACGRPOATAVYKVEYARFGVPVIADGIIQ 368
Db 299 QAENLIQAGVDGLRVGMGSGSICTQEVCAVRGOATAVYVNSLIAKSGVPVIADGIS 358
QY 369 NVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAMDHLSSQN 428
Db 359 NSGHIKALSLGASTVMGSLAATTEAPGAYVYQNGQVRVKKYRGMSLEAMTK--GSDA 416
QY 429 RYFSEADKIKVAQVSGAVQDKGSIHKFVPLIAGIQHSCQDIGAASLTQVRAMYSSEL 488
Db 417 RYLGDTAKLKIAGVVGAVKDKGSVLFNFIPTYLQAVRQGFQDIGASSLSQSAHDLRSREL 476
QY 489 KFEKRTSSAQVEGVHSLHSYEKRLF 514
Db 477 RLEVRSGAAQVEGVHGLVSYEKKYF 502

RESULT 10
Q9AY75 PRELIMINARY; PRT; 501 AA.
AC Q9AY75;
DT 01-JUN-2001 (Tremblrel. 17, Created).
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative inosine monophosphate dehydrogenase.
GN OSJNBA0091J19.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;

RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
RT "Oryza sativa chromosome 3 BAC OSJNBA0091J19 genomic sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084320; AAK09225.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR01093; IMPdh/GMPrtase.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 1.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 501 AA; 52655 MW; DDE295CB714C3802 CRC64;

Query Match 42.6%; Score 1117; DB 10; Length 501;
Best Local Similarity 47.2%; Pred. No. 1.2e-69;
Matches 247; Conservative 80; Mismatches 160; Indels 36; Gaps 9;

QY 6 ISGTSYVPDGLTAQQLFNCGDGLTYNDLFLIPGYIDFTADQVDLTSAITKTKITLTP 65
Db 1 MAASSADLADDCFPAPRLFSQGSVSYTYDDVIFLPGYIGFPADAVDLSTLSRRIPLSIPC 60
QY 66 VSSPMDTVTEAGMAIAMALTGGIGFIHNCPTPEFOANEVRKVKYEQGFITDPVVLSPK 125
Db 61 VASPMDTVSEAMAAAMASLGAADVHNCNTEPHLOASIVRAAKSRRLPFVSSVPLFSPAS 120
QY 126 --RVRDVFEAKARHFGCIPITDTGRMGSRVLGI----ISSRIDFLKEEHDCLFEEI 178
Db 121 TPSLSDF---AGHDY-GL-VTERGDSLKLGVAVAAETSSR-----QAP 160
QY 179 MTKREDLVVAPRSIT---LKEANEILORSKKGLPIVNEDELVAIARTDLKKNRDYP 234
Db 161 LPVSEYMRPAPRSVSASFDEQAAAFADDEGLDYAPLVSDSEVIDLITVNDVERIRSY 220
QY 235 LASK--DAKKQLLGAAGIETHEDDKYRLDLLAQAGVDVVLDSQGSNIFQIMIKYIK 291
Db 221 KLGPSTLGADKFFVVAASIGTREDDKRLLEQLVKAGANAIWVDSQGSNIYQIDMIKYAK 280
QY 292 DKYPNLQYIGNVVTAQAQAKNLIDAGVDALRVGMGSGSICIIOEVLACGRPOATAVYK 351
Db 281 KMYPEVDLIGNVVTIAQAQNLVAVSGVDGLRVGMGSGSICTQEVCAVRGOATAVYKVA 340
QY 352 EYARFVGVPVIADGCIQNVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKY 411
Db 341 SYAKDHNVPVIADGIGISNSGHIKALSLGASTVMGSLAATTEAPGEYFFSDGIRLKKY 400
QY 412 RGMGLDAMDHLSSQNRIFYSEADKIKVAQVSGAVQDKGSIHKFVPLIAGIQHSCQDI 471
Db 401 RGMGLLEAMTK--GSDARYLGDTLKLKVAQVVGAVADKGSVLRFLIPTMQAVKQGFQDL 458
QY 472 GAKSLTQVRAMYSSELKFEKRTSSAQVEGVHSLHSYEKRLF 514
Db 459 GASSLSQSAHELRLSEFTIKLEVRTGAQVEGGIHLVSYEKKAF 501

RESULT 11
Q8RC64 PRELIMINARY; PRT; 484 AA.
AC Q8RC64;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE IMP dehydrogenase/GMP reductase.
GN GUAB OR TTE0582.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;

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RN {}
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013027; AAM23853.1; -.
KW Complete proteome.
SQ SEQUENCE 484 AA; 52460 MW; 6531013B9BD78EA9 CRC64

Query Match 37.2%; Score 973; DB 16; Length 484;
Best Local Similarity 45.1%; Pred. No. 1.2e-59;
Matches 216; Conservative 89; Mismatches 160; Indels 14; Gaps 5;

QY 28 DGLTYNDFLLPGYIDFTADQVDLTSLTKKITLKTPLVSSPMDVTEAGMAIAMALTG 87
Db :|||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
8 EGLTFDDVLLIPAKSDVLPKDVLDKTRLTTKITLNLPLMSAGMDVTEALAIAREGG 67

QY 88 IGFTHHNTPEFOANEVRKVKYEOGFITDPVVLSPKDRVDFEAKAHGFCGIPITDT 147
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
68 IGVTHKMSIEROAMEVDKVRSEHGVIITDPFSLSPDHTTRDAELMAYKISGVPI-- 125

QY 148 GRMGRIVGITSSRDIDFLKEEHDFLEIMTKREDLVVAPRSITLIKANEILORSKKG 207
Db : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
126 --VDSKLVGITNRDIRF--EDDLDKPIREVMTK--ENLVTAAPGTTLEAKQILKKHIE 180

QY 208 KLPVNEDELVAIIARTDLKKNRDYPLASKDAKKQLLCAIGTHEDKYRLDLAQAG 267
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 KLPVDENNVLKGLITIKDIEKAVEFPNAKDEKGRLLVAAAVGVCKDMDRVKALIEAG 240

QY 268 VDVVVLDSQGSNIFQINMIKIKDKYPNLQVIGNVVTAQAQAKNLIDGVDALRVGMS 327
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 VDAIVVDTAHGSTRVLDAVAKIKEKYPDVQLIAGNVATAEATRDLEIGADAVKVGICP 300

QY 328 GSICIIQEVLAGCRPOATAVVKYEVYARFGVPVIADGIONVGHIAKLALGASTVMG 387
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 GSICITRVVAGVGPQITAIYECAKEADKYGIPVIADGIIKYSGDIVKIAAGASVVMIG 360

QY 388 SLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSONRYFSEADIKVAQGVSGA 447
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 SLFAGTEESPEIEITYQGRSYKVRGMGSLGAMKE--GSSDRYFOEEAKLVEGVEGRV 418

QY 448 QDKGSIHKFVPLYLAGIOHSCODIGAKSLTQVRAMYSGELKFEKRTSAQVEGVHSL 506
Db : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
419 PYRGPRLRETVYOLIGLIRAGMCGCVKNIEELRT----KTKFVRITQGLIESHPHDI 472

RESULT 12
Q9PNN3 PRELIMINARY; PRT; 485 AA.
ID Q9PNN3;
AC Q9PNN3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)
GN GUAB OR CJ1058C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Pen C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
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RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL: AL139077; CAB73314.1; -.
DR HSSP; P12268; 1B3O.
DR InterPro; IPR000544; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPDH/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMs; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52151 MW; 63433266B963CDF CRC64;

Query Match 36.9%; Score 966.5; DB 16; Length 485;
Best Local Similarity 45.6%; Pred. No. 3.5e-59;
Matches 219; Conservative 78; Mismatches 164; Indels 19; Gaps 8;

QY 30 LTYNDFLLPGYIDFTADQVDLTSLTKKITLKTPLVSSPMDVTEAGMAIAMALTGIG 89
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
8 LTFEDVLLRPGYSEVLPKREKVIHTKLTNITLNMPLISAMDTVTEHRAAIMARLGIG 67

QY 90 FIHHNCTPEFOANEVRKVKYEOGFITDPVVLSPKDRVDFEAKARHGFSGIPITDGR 149
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
68 VTHKNMDIASQVREVRKVKSSGVIIIDPIFVSPKASVAEALIEIMAEYRISGVPVDEDK 127

QY 150 MGSRLVGISSRDIDFLKEEHDFLEIMTKREDLVVAPRSITLKEANEILORSKKGKL 209
Db : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
128 ---KLIGILTNRDLRF--ESDSNLVENVMTKM--PLITAPKCGCTLDDAEKIFSTNKEKL 181

QY 210 PIVNEDELVAIIARTDLKKNRDYPLASKDAKKQLLCAIGTHEDDKYRLDLAQAGVD 269
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
182 PIVDEQGRLEGGLITIKDKRKREYPDANKDNFGLRVGAIGVGQMD--RVDALVEAGVD 239

QY 270 VVVLDSQGSNIFQINMIKIKDKYPNLQVIGNVVTAQAQAKNLIDAGVDALRVGMSGS 329
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
240 VVVLDSAHGHSKGIIDTVKAIKAKYPNLIDLAGNIATTAATAAKALCEAGVDVAVKVGICPGS 299

QY 330 ICIIQEVLAGCRPOATAVVKYEVYARFGVPVIADGIONVGHIAKALALGASTVMGSL 389
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
300 ICTTRIVSGVGPQISAIDECVEEANKFGVPVIADGIIKYSGDIAKALAVGASSVMIGSL 359

QY 390 LAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSONRYFSEA--DKIKVAQGVSGA 446
Db || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
360 LAGIDESPGELFTYQGRQYRSYRGMGSLGAMOK--GSSDRYFOQGTADQKL--VPEGIEGR 416

QY 447 VQDKGSIHKFVPLYLAGIOHSCQDIGAKSLTQVRAMYSGELKFEKRTSSAQVEGVHSL 506
Db : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
417 VPYVGSIRSVVHQLLGLRSMGYGAKDIED-----FOKRAEFVEITTAGLKESHVHDV 471

RESULT 13
Q97FM8 PRELIMINARY; PRT; 485 AA.
ID Q97FM8;
AC Q97FM8;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE IMP dehydrogenase.
GN CAC2701.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
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RA	Bennett G.N., Koonin E.V., Smith D.R.;
RT	"genome sequence and comparative analysis of the solvent-producing
RT	bacterium Clostridium acetobutylicum.";
RL	J. Bacteriol. 183:4823-4838(2001).
DR	EMBL; AE007768; AAK80647.1; -.
DR	InterPro; IPR000644; CBS_domain.
DR	InterPro; IPR003009; FMN_enzyme.
DR	InterPro; IPR001093; IMPdh/GMPrtase.
DR	Pfam; PF00571; CBS; 2.
DR	Pfam; PF00478; IMPDH_C; 1.
DR	Pfam; PF01574; IMPDH_N; 1.
DR	SMART; SM00116; CBS; 2.
DR	TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW	Complete proteome.
SQ	SEQUENCE 485 AA; 52188 MW; 994D1C5347F7A267 CRC64;
<hr/>	
Query Match	36.6%; Score 958; DB 16; Length 485;
Best Local Similarity	44.2%; Pred. No. 1.4e-58;
Matches 212; Conservative	86; Mismatches 164; Indels 18; Gaps 5;

QY 1 IHNMTIAEQASEVDRVKRQENGVIITNPISLSKDNSVQEQALDLMKRYRISGVPIITDN--- 126
 Db 70 IHNMTIAEQASEVDRVKRQENGVIITNPISLSKDNSVQEQALDLMKRYRISGVPIITDN--- 126
 QY 151 GSRLVGIISSRDIDFLKEEHDCFLEEIIMTKREDLVVAPRSTLKEANEILQRSKKGKLP 210
 Db 127 AGKLIGIITNRDIVE--ETDYSKKEIEELMT--TENLVTAPOGTTIDEAKNLKKHKEIKLP 183
 QY 211 IVNDELVAIARTDLKKRDYPLASKDAKKQLLCGAIGTHEDDKYRLDLLAQAGVDV 270
 Db 184 LVDENFVLKGLITIKDIEKIRKFPNAKADSQGRLLCGAGVGVTKMDMDRVKALVDASVDV 243
 QY 271 VVLDSSQGSNIFQINMIKYIKDKYPNLÖVIGGNVTTAAQAKNLIDAGVDALRVGMSGSI 330
 Db 244 IVLDTAHGSQGVLEAVKTIKKAYPELÖVTAGNVATAAAVHDLIEAGADCVKVIGPGSI 303
 QY 331 CLIQEVLACGRPOATAVVKVEYARFEGVPVIADGGIÖNVGHIAKALALGASTVMMGSL 390
 Db 304 CTRRVVAGIGVPQLTAVMDCVEANKYGVPIIADGKIKYSGDIYKALAAKAVMMGSMF 363
 QY 391 AATTEAPGEYFFSDGIRLKKYRGMSLDAMDKHLSSÖNRYFSEADKIKVAQGVSGAVÖDK 450
 Db 364 AGCEEAPGETEITYÖGRSTYKVRGMSLAAM--ÖCGSKDRYFQEGNKKLVPGEVGRVPFK 421
 QY 451 GSIHKFVPLYIAGIQHSCÖDIGAKSLTÖVRAMMYSGELKFEKRTSSAQVEGVSHLSYE 510
 Db 422 GSVIETVFQILGIRSGMGYLGSRNMTL-----FEKATFVVQTSAGLRESHPHD 471
 RESULT 14
 Q8XZG6
 ID Q8XZG6 PRELIMINARY; PRT; 487 AA.
 AC Q8XZG6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Probable inosine-5'-monophosphate dehydrogenase oxidoreductase protein
 (EC 1.1.1.205).
 GN GUAB OR RSC1429 OR RS05263.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 CC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigurier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";
RL Nature 415:497-502(2002).
DR EMBL; AL646064; CAD15131.1; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPdh/GMPrtase.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMs; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 487 AA; 52065 MW; A4052A61119CF011 CRC64;

	Query Match	35.9%; Score 941.5; DB 16, Length 487;
	Best Local Similarity	42.7%; Pred. No. 2e-57;
	Matches	206; Conservative 87; Mismatches 170; Indels 19; Gaps 6;
QY	30 LTYNDFLILPEGYIDFTADQVDLTSLTKKTLTKTPLVSSPMDVTYEAGMAIAMLTTGGIG	89
Dd	8 LTFDDVLVFAISAVLPRDTSLRKTLLRTIELAIPLVSAAMDVTEARLAITAMAQQGGIG	67
QY	90 FIHNCTPEEQANEVRKKVKKYEOGFTDPVLSPKDRVDRVFEAKARHFGCIPITDTGR	149
Dd	68 IVHKNLKPREEQAREVAKVKKRFESGVLRDPITIGPDMKVDRVMALSAQHGISEGPVLE--	124
QY	150 MGSRLVGIISSRDIDFLKEEHCDFLEIMTKREDLVVAPRSITLKEANEILORSKKGKL	209
Dd	125 -GNKVVGLITNRDLRf--EELDAPYAKMTPGEKLVTVREGASLSEAKRLMNKHRLERV	181
QY	210 PIVNEDELVAIIARTDLKKNRDYPPLASKDAKKQLLGCAALGTHEDDKYRLDLLAAQAVD	269
Dd	182 LVVDGNFELRGSLITVKDIQKATEHPPLASKDERGSLRVGAAYGVGPNDLRAVDLLVKAGVD	241
QY	270 VVVLDSQGSNIFFQINMIKYIKDKYPNLQVIGNVVTAQAQKNLIDAGVDALRVGMSSGS	329
Dd	242 VIVVDTAHGHSQGVLRSVRWIKDKPYOVYIGNIATAEAAKALVDHGADVKKVGIGPGS	301
QY	330 ICIIQEVLACGRPOATAVYKVEYARRRGVPVIADGGIQNVGHIALALAGASTVMMSGSL	389
Dd	302 ICTTRIVAGVGPQISAVSNVAEALKNTGVPVLVADGVRYSGDIAKALAAGHTVMMGSM	361
QY	390 LAATTEAPGEYEFSDGIRLKRYRGMGSLDAMDKHLSSQNRYFSE-----ADKIKVAQCVS	444
Dd	362 FAGTEEPAGEVFELYQGRSYKSYRGMGSGVAMKD--GAADRYFQEDNTANVDKL-VPEGIE	418
QY	445 GAVODKGSIHKEFPYPILAGIQHSCQDIGAKSLTQVRAMMYSGELKEFKRTSSAQVEGVH	504
Dd	419 GRVPYKGSVIPVHQLTGGRSSMGYCGCASIAE----WHEKSQFOVQITAAGMRSHVH	473
QY	505 SL 506	
Dd	474 DV 475	
RESULT	15	
Q9KGN8	PRELIMINARY;	PRT; 485 AA.
AC Q9KGN8;		
DT 01-OCT-2000 (TREMBLrel. 15, Created)		
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE Inositol-monophosphate dehydrogenase (EC 1.1.1.205).		
GN GUAB OR BH0020.		
OS Bacillus halodurans.		
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;		
OC Bacillaceae; Bacillus.		

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 01:37:31 ; Search time 19 Seconds
(without alignments)
546.637 Million cell updates/sec

Title: US-09-846-637C-4
Perfect score: 2619
Sequence: 1 MADYLISGGSYVPDDGLTA.....SSAQVEGGVSLHSYEKRLF 514

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2595	99.1	514	1	IMD2_HUMAN	P12268 homo sapien
2	2559	97.7	514	1	IMD2_MESAU	P12269 mesocricetu
3	2555	97.6	514	1	IMD2_MOUSE	P24547 mus musculu
4	2222	84.8	514	1	IMD1_HUMAN	P20839 homo sapien
5	2203	84.1	514	1	IMD1_MOUSE	P50096 mus musculu
6	1764.5	67.4	537	1	IMDH_DROME	O07152 drosophila
7	1610.5	61.5	524	1	IMD4_YEAST	P50094 saccharomyc
8	1607.5	61.4	523	1	IMD3_YEAST	P50095 saccharomyc
9	1605.5	61.3	521	1	IMH3_CANAL	O00086 candida alb
10	1589.5	60.7	523	1	IMD2_YEAST	P38697 saccharomyc
11	1473.5	56.3	524	1	IMDH_SCHPO	O14344 schizosacch
12	1414	54.0	454	1	IMDH_PNECA	O12658 pneumocysti
13	1385.5	52.9	512	1	IMDH_TRYBB	P50098 trypanosoma
14	1371.5	52.4	514	1	IMDH_LEIDO	P21620 leishmania
15	1155	44.1	502	1	IMH2_ARATH	O9sa34 arabidopsis
16	1106.5	42.2	503	1	IMH1_ARATH	P47996 arabidopsis
17	1043.5	39.8	403	1	IMD1_YEAST	P39567 saccharomyc
18	952	36.3	490	1	IMDH_AQUAE	O67820 aquifex aeo
19	887.5	33.9	513	1	IMDH_BACSU	P21879 bacillus su
20	857.5	32.7	488	1	IMDH_ACICA	P31002 acinetobact
21	849.5	32.4	529	1	IMDH_MYCTU	O50715 mycobacteri
22	839.5	32.1	529	1	IMDH_MYCLE	O49729 mycobacteri
23	837	32.0	488	1	IMDH_ECOLI	P06981 escherichia
24	836	31.9	488	1	IMDH_HAEIN	P44334 haemophilus
25	827.5	31.6	521	1	IMDH_CHLVI	O50316 chlorobium
26	811	31.0	481	1	IMDH_HELPI	P56088 helicobacte
27	811	31.0	487	1	IMDH_PASMU	O916b7 pasteurella
28	809	30.9	481	1	IMDH_HELPJ	O92114 helicobacte
29	808	30.9	492	1	IMDH_STRPY	P50099 streptococc
30	772	29.5	498	1	IMDH_RHITR	O9kh33 rhizobium t
31	770	29.4	496	1	IMDH_METJA	O59011 methanococc
32	704.5	26.9	485	1	IMDH_PYRFU	P42851 pyrococcus
33	689.5	26.3	485	1	IMDH_PYRAB	O9uy49 pyrococcus

34	684	26.1	486	1	IMDH_PYRHO	O58045 pyrococcus
35	618	23.6	404	1	IMDH_BORBU	P49058 borrelia bu
36	582.5	22.2	503	1	IMDH_TRIFO	P50097 tritrichomo
37	463	17.7	479	1	YI43_MYCTU	O50591 mycobacteri
38	437	16.7	478	1	YI43_MYCLE	O32912 mycobacteri
39	326	12.4	345	1	GUAC_HUMAN	P36959 homo sapien
40	323.5	12.4	356	1	GUAC_ASCSU	P27442 ascaris suu
41	317	12.1	345	1	GUAC_RAT	O92244 rattus norv
42	315.5	12.0	358	1	GUAC_CAEL	O16294 caenorhabdi
43	293	11.2	346	1	GUAC_ECOLI	P15344 escherichia
44	292	11.1	349	1	GUAC_BUCAI	P57300 buchnera ap
45	166	6.3	265	1	Y188_METJA	O57647 methanococc

ALIGNMENTS

RESULT 1	
IMD2_HUMAN	
ID	IMD2_HUMAN
AC	P12268; STANDARD; PRT; 514 AA.
DT	01-OCT-1989 (Rel. 12, Created)
DT	01-MAY-1991 (Rel. 18, last sequence update)
DT	16-OCT-2001 (Rel. 40, last annotation update)
DE	Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP dehydrogenase 2) (IMPDH-II) (IMPD 2).
DE	IMPDH2 OR IMPD2.
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
OX	[1]
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX	MEDLINE=89008491; PubMed=2902093;
RA	Collart F.R., Huberman E.;
RT	"Cloning and sequence analysis of the human and Chinese hamster inosine-5'-monophosphate dehydrogenase cDNAs.";
RT	J. Biol. Chem. 263:15769-15772(1988).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Spleen;
RC	MEDLINE=90203022; PubMed=1969416;
RX	Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
RA	"Two distinct cDNAs for human IMP dehydrogenase.";
RT	J. Biol. Chem. 265:5292-5295(1990).
RL	[3]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Blood;
RC	MEDLINE=95091778; PubMed=7999076;
RX	Glesne D.A., Huberman E.;
RA	"Cloning and sequence of the human type II IMP dehydrogenase gene.";
RT	Biochem. Biophys. Res. Commun. 205:537-544(1994).
RL	[4]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=95204479; PubMed=7896827;
RX	Zimmermann A.G., Spychala J., Mitchell B.S.;
RA	"Characterization of the human inosine-5'-monophosphate dehydrogenase type II gene.";
RT	J. Biol. Chem. 270:6808-6814(1995).
RL	[5]
RN	CHARACTERIZATION.
RP	MEDLINE=95283610; PubMed=7763314;
RX	Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
RA	"Recombinant human inosine monophosphate dehydrogenase type I and type II proteins. Purification and characterization of inhibitor binding.";
RT	Biochem. Pharmacol. 49:1323-1329(1995).
RL	[6]
RN	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP	MEDLINE=99199217; PubMed=10097070;
RX	Colby T.D., Vanderveen K., Strickler M.D., Markham G.D., Goldstein B.M.;
RA	"Crystal structure of human type II inosine monophosphate

RT dehydrogenase: implications for ligand binding and drug design.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3531-3536(1999).
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
CC -1- CATALYTIC ACTIVITY: inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL
CC LEUKOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: J04208; AAA36112.1; -.
DR EMBL: L33842; AAA67054.1; -.
DR EMBL: L39210; AAB70699.1; -.
DR PIR: A31997; A31997.
DR PIR: B35566; B35566.
DR PDB: 1B3O; 12-APR-99.
DR Genew: HGNC:6053; IMPDH2.
DR MIM: 146691; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMPDH/GMPrtase.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR TIGRfams: TIGR01302; IMP_dehydrog; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain; 3D-structure.
FT DOMAIN 112 167 CBS 1.
FT DOMAIN 177 232 CBS 2.
FT BINDING 331 331 IMP (POTENTIAL).
FT CONFLICT 190 191 AG -> RS (IN REF. 1).
SQ SEQUENCE 514 AA; 55805 MW; 876BEA0EC1DBEE9 CRC64;

Query Match 99.1%; Score 2595; DB 1; Length 514;
Best Local Similarity 99.2%; Pred. No. 3.6e-168;
Matches 510; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADYLISGTSYVPDDGLTAQQLFNCGDLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
Db 1 MADYLISGTSYVPDDGLTAQQLFNCGDLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLVSSPMDVTEAGMAIAMLTGIGIFIHNCPTPEQANEVRKVKYEQGFITDPVY 120
Db 61 LKTPLVSSPMDVTEAGMAIAMLTGIGIFIHNCPTPEQANEVRKVKYEQGFITDPVY 120
QY 121 LSPKDRVDFEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCLFEETMT 180
Db 121 LSPKDRVDFEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCLFEETMT 180
QY 181 KREDLVAPRSITLKEANEILQRSKKGKLPVINEDEDELVAIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVAPAGITLKEANEILQRSKKGKLPVINEDEDELVAIARTDLKKNRDYPLASKDA 240
QY 241 KKOLLGGAIGTHEDDKYRLDLAQAQGVDDVVLDSQGSNIFQINMIKIKDKYPNLOVI 300
Db 241 KKOLLGGAIGTHEDDKYRLDLAQAQGVDDVVLDSQGSNIFQINMIKIKDKYPNLOVI 300

QY 301 GGNVYTAQAQAKNLIDAGVDALRVGMSSGICITQEVLIACGRPOATAVYKVEYARREGVP 360
Db 301 GGNVYTAQAQAKNLIDAGVDALRVGMSSGICITQEVLIACGRPOATAVYKVEYARREGVP 360
QY 361 VIADGCIQNVGHIAKALALCASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGCIQNVGHIAKALALCASTVMGSLLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRIFYSEADKIKYAQGVSGAVQDKGSIHKFVYLLAGIQHSCQDIGAASLTQVR 480
Db 421 DKHLSSQNRIFYSEADKIKYAQGVSGAVQDKGSIHKFVYLLAGIQHSCQDIGAASLTQVR 480
QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514
Db 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514

RESULT 2
IMD2_MESAU STANDARD; PRT; 514 AA.
ID P12269;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
DE dehydrogenase 2) (IMPDH-II) (IMPD 2).
GN IMPDH2 OR IMPDH.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 336-370.
RX MEDLINE=89008491; Pubmed=2902093;
RA Collart F.R., Huberman E.;
RT "Cloning and sequence analysis of the human and Chinese hamster
RT inosine-5'-monophosphate dehydrogenase cDNAs.";
RL J. Biol. Chem. 263:15769-15772(1988).
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
CC -1- CATALYTIC ACTIVITY: inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04209; AAA36993.1; -.
DR PIR: B31997; B31997.
DR HSSP: P12268; 1B3O.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMPDH/GMPrtase.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR TIGRfams: TIGR01302; IMP_dehydrog; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;

KW	Multigene family; Repeat; CBS domain.			
FT	DOMAIN	112	167	CBS 1.
FT	DOMAIN	177	232	CBS 2.
FT	BINDING	331	331	IMP (POTENTIAL).
SO	SEQUENCE	514 AA;	55890 MW;	5FA0138FA41E8A02 CRC64;
Query Match				
Best Local Similarity		97.78;	Score 2559;	DB 1; Length 514;
Matches 504;		Conservative 3;	Mismatches 7;	Indels 0; Gaps 0;
QY	1	MADYLIISGGSYVPDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSALTKKIT	60	
Db	1	MADYLIISGGSYVPDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSALTKKIT	60	
QY	61	LKTPLVSSPMDVTVEAGMAIAMALTGIGIFIHNCTPEFQANEVRKVKYEQGFTDPV	120	
Db	61	LKTPLVSSPMDVTVEAGMAIAMALTGIGIFIHNCTPEFQANEVRKVKYEQGFTDPV	120	
QY	121	LSPKDRYRVDFEAKARHGFSGIPITDTGRMGSRVLVGIISSRDIDFLKEEHDCLFLEEIMT	180	
Db	121	LSPKDRYRVDFEAKARHGFSGIPITDTGRMGSRVLVGIISSRDIDFLKEEHDCLFLEEIMT	180	
QY	181	KREDLVVAPRSITLKEANEILORSKKGKPLPIVNEDELVAIARTDLKKNRDYPLASKDA	240	
Db	181	KREDLVVAPRSITLKEANEILORSKKGKPLPIVNEDELVAIARTDLKKNRDYPLASKDA	240	
QY	241	KKQLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIYIKDKYPNLQVI	300	
Db	241	KKQLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIYIKDKYPNLQVI	300	
QY	301	GGNVVTAQAQAKNLIDAGVDALRVGMSGISICITIOEVLACGRPOATAVKVEYARRFQV	360	
Db	301	GGNVVTAQAQAKNLIDAGVDALRVGMSGISICITIOEVLACGRPOATAVKVEYARRFQV	360	
QY	361	VIADGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRKKYRGMSLDAM	420	
Db	361	VIADGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRKKYRGMSLDAM	420	
QY	421	DKHLSSQNRFESEADKIKVAQGVSAVQDKGSIHKFVPLYIAGIOHSDIGAKSLTQVR	480	
Db	421	DKHLSSQNRFESEADKIKVAQGVSAVQDKGSIHKFVPLYIAGIOHSDIGAKSLTQVR	480	
QY	481	AMMYGSELKFEKRTSSAQVEGVSLSHYEKRLE	514	
Db	481	AMMYGSELKFEKRTSSAQVEGVSLSHYEKRLE	514	

RT	dehydrogenase associated with cellular resistance to mycophenolic acid.";			
RT	Biochim. Biophys. Acta 1217:156-162(1994).			
CC	-!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.			
CC	-!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O = xanthosine 5'-phosphate + NADH.			
CC	-!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.			
CC	-!- SUBUNIT: HOMOTETRAMER.			
CC	-!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP REDUCTASE.			
CC	-!- SIMILARITY: CONTAINS 2 CBS DOMAINS.			
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CC	EMBL; M33934; AAA39311.1; -.			
DR	EMBL; M98333; AAA20181.1; -.			
DR	PIR; JT0565; JT0565.			
DR	HSSP; P12268; 1B3O.			
DR	PMAA-2DPAGE; P24547; -.			
DR	MGD; MGI:109367; Impdh2.			
DR	InterPro; IPR000644; CBS_domain.			
DR	InterPro; IPR003009; FMN_enzyme.			
DR	InterPro; IPR001093; IMPdh/GMPase.			
DR	Pfam; PF00478; IMPDH_C; 1.			
DR	Pfam; PF00571; CBS; 2.			
DR	Pfam; PF01574; IMPDH_N; 1.			
DR	SMART; SM00116; CBS; 2.			
DR	TIGRFAMS; TIGR01302; IMP_dehydrog; 1.			
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.			
KW	Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;			
KW	Multigene family; Repeat; CBS domain.			
FT	DOMAIN	112	167	CBS 1.
FT	DOMAIN	177	232	CBS 2.
FT	BINDING	331	331	IMP (POTENTIAL).
FT	VARIANT	333	333	T -> I (IN MYCOPHENOLIC ACID RESISTANT CELLS).
FT	VARIANT	351	351	S -> Y (IN MYCOPHENOLIC ACID RESISTANT CELLS).
FT	CONFLICT	483	483	T -> M (IN REF. 2).
FT	SEQUENCE	514 AA;	55785 MW;	D5B66A5C5EBCC421 CRC64;
Query Match				
Best Local Similarity		97.68;	Score 2559;	DB 1; Length 514;
Matches 503;		Conservative 4;	Mismatches 7;	Indels 0; Gaps 0;
QY	1	MADYLIISGGSYVPDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSALTKKIT	60	
Db	1	MADYLIISGGSYVPDDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSALTKKIT	60	
QY	61	LKTPLVSSPMDVTVEAGMAIAMALTGIGIFIHNCTPEFQANEVRKVKYEQGFTDPV	120	
Db	61	LKTPLVSSPMDVTVEAGMAIAMALTGIGIFIHNCTPEFQANEVRKVKYEQGFTDPV	120	
QY	121	LSPKDRYRVDFEAKARHGFSGIPITDTGRMGSRVLVGIISSRDIDFLKEEHDCLFLEEIMT	180	
Db	121	LSPKDRYRVDFEAKARHGFSGIPITDTGRMGSRVLVGIISSRDIDFLKEEHDCLFLEEIMT	180	
QY	181	KREDLVVAPRSITLKEANEILORSKKGKPLPIVNEDELVAIARTDLKKNRDYPLASKDA	240	
Db	181	KREDLVVAPRSITLKEANEILORSKKGKPLPIVNEDELVAIARTDLKKNRDYPLASKDA	240	
QY	241	KKQLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIYIKDKYPNLQVI	300	
Db	241	KKQLCGAAIGTHEDDKYRLDLLAAGVDVVLDDSSQGSNIFQINMIYIKDKYPNLQVI	300	

```

OY 301 GGNVTTAAQAKNLIDAGVADLRVGMGSGSICITQEVLAACGRPQATAVYKVEYARRECV 360
DB 301 GGNVTTAAQAKNLIDAGVADLRVGMGSGSICITQEVLAACGRPQATAVYKVEYARRECV 360
OY 361 VIADGGIQNVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDM 420
DB 361 VIADGGIQNVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDM 420
OY 421 DKHLSSQNRFFSEADKIKYAGVSGAVODKSGIHKFVPLYIAGIQHSCODIGAKSLTQVR 480
DB 421 DKHLSSQNRFFSEADKIKYAGVSGAVODKSGIHKFVPLYIAGIQHSCODIGAKSLTQVR 480
OY 481 AMYSGELKFEKRTSSAQVEGVSLSHSYEKRLF 514
DB 481 AMYSGELKFEKRTSSAQVEGVSLSHSYEKRLF 514

RESULT 4
IMD1_HUMAN
ID IMD1_HUMAN STANDARD; PRT; 514 AA.
AC P20839;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP
DE dehydrogenase 1) (IMPDH-1) (IMPD 1).
DE IMPDH OR IMPD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=90203022; PubMed=1969416;
RA Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
RT "Two distinct cDNAs for human IMP dehydrogenase.";
RL J. Biol. Chem. 265:5292-5295(1990).
[2]
RP CHARACTERIZATION.
RX MEDLINE=95283610; PubMed=7763314;
RA Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
RT "Recombinant human inosine monophosphate dehydrogenase type I and
RT type II proteins. Purification and characterization of inhibitor
RT binding.";
RL Biochem. Pharmacol. 49:1323-1329(1995).
CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL
CC LEUKOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J05272; AAA36114.1; ALT_SEQ.
DR PIR: A35566; A35566.
DR HSSP: P12268; 1B30.
DR Genew; HGNC:6052; IMPDH1.

```

DR	MM; 146690; -	CBS_domain.
DR	InterPro; IPR000644;	CBS_domain.
DR	InterPro; IPR003009;	FMN_enzyme.
DR	InterPro; IPR001093;	IMPdh/GMPrtase.
DR	Pfam; PF00478;	IMPdh_C; 1.
DR	Pfam; PF00571;	CBS; 2.
DR	Pfam; PF01574;	IMPdh_N; 1.
DR	SMART; SM00116;	CBS; 2.
DR	TIGRFAMS; TIGR01302;	IMP_dehydrog; 1.
DR	PROSITE; PS00487;	IMP_DH_GMP_RED; 1.
KW	Oxidoreductase; NAD; GMP biosynthesis;	Purine biosynthesis;
KW	Multigene family; Repeat;	CBS domain.
FT	DOMAIN	112 167 CBS 1.
FT	DOMAIN	177 232 CBS 2.
FT	BINDING	331 331 IMP (POTENTIAL).
SEQ	SEQUENCE	514 AA; 55449 MW; 751303F8E9E21061 CRC64;
Query Match		
Best Local Similarity		
Matches		
427; Conservative		
39; Mismatches		
48; Indels		
0; Gaps		
0;		
QY	1	MADYLLISGGSYVPPDDGLTAQQLFNCGDGLTYNDLFLILPGYIDFTADQVDLTSLTKKIT 60
Db	1	MADYLLISGGTGYVPEPDLTAQQLFASADDLTYNDLFLILPGYIDFTADEVDLTSLTKKIT 60
QY	61	LKTPLVSSPMDVTVEAGMAIAMLTCGIGFIHNCTPEFOANEVKKYKEOGFITDPV 120
Db	61	LKTPLISSPMDVTVEADMAIAMALMGIGFIHNCTPEFOANEVKKYKEOGFITDPV 120
QY	121	LSPKDRVDVFEAKARHGFEGIPITDTGRMGSRVLGIISSRDIDFLKEEHDFLEIMT 180
Db	121	LSPSHTVGDVLEAKMRHGFSGIPITETGTGMSKLVGIVTSRIDIDFLAEKDHDTLLSEVMT 180
QY	181	KREDLVAPRSITLKEANEILORSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
Db	181	PRIELVAPAGVTLKEANEILORSKKGKLPVNDCELVAAIARTDLKKNRDYPLASKDS 240
QY	241	KKOLLGGAIGTHEDDKYRLDLLAQAGVDVVLDSQGSNIFQIMIKYIKDKYPNLOVI 300
Db	241	QKOLLGGAAGVTRREDDKYRLDLLTQAGVDVIVLDSQGSNSVQIAMVHIKQYPHLOVI 300
QY	301	GGNVTTAAQAKNLIDAGVDALRVGSGSICIIQEVVLACGRPOATAVYKVEYARFGVP 360
Db	301	GGNVTTAAQAKNLIDAGVDGLRVGSGSICITQEVMAACGRPOGTAVYKVAEYARFGVP 360
QY	361	VIADGCIQNVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db	361	VIADGCIQTVGHVVKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY	421	DKHLSSQNRYSFSEADKIKVAQVGSAGVODKSGIHKFVYPYLIAGIOHSCODIGAKSLTQVR 480
Db	421	EKSSSSQKRYFSEGDKVKIAQVSGSIQDKSGIQKFVYPYLIAGIQHGCODIGARSLTVLR 480
QY	481	AMMYSGELKFEKRTSSAQVEGVSLSHYEKL 514
Db	481	SMMYSGELKFEKRTMSAQIEGVHGLSHYEKRLY 514
RESULT 5		
IMD1_MOUSE		
ID	IMD1_MOUSE	STANDARD; PRT; 514 AA.
AC	P50096;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	01-NOV-1997 (Rel. 35, Last annotation update)	
DE	Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP	
DE	dehydrogenase 1) (IMPDH-1) (IMPD 1).	
GN	IMPDH1.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	

RP SEQUENCE FROM N.A.
RC TISSUE=Leukemia;
RA Dayton J.S., Mitchell B.S.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
CC -|- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -|- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -|- SUBUNIT: HOMOTETRAMER.
CC -|- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -|- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL: U00978; AAA18285.1; .
DR HSSP: P12268; 1B3O.
DR MGD: MGI:96567; Impdh1.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMPdh/GMPrtase.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR TIGRFAMS: TIGR01302; IMP_dehydrog; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 112 167 CBS 1.
FT BINDING 177 232 CBS 2.
FT BINDING 331 331 IMP (POTENTIAL).
SQ SEQUENCE 514 AA; 55294 MW; B38AA2EB0ECC4CE CRC64;

Query Match 84.1%; Score 2203; DB 1; Length 514;
Best Local Similarity 82.5%; Pred. No. 1.le-141;
Matches 424; Conservative 39; Mismatches 51; Indels 0; Gaps 0;

QY 1 MADYLISGGSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDTLSALTKKIT 60
DB 1 MADYLISGGTGYPEDGLTAHELFLANADGLTYNDFLILPGFIDFADENVDTLSALTKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMAITGIGIFIHNCPTPEQANEVRKVEKYEOGFITDPVV 120
DB 61 LKTPLVSSPMDVTVEADMAIAMAIMGIGIFIHNCPTPEQANEVRKVEKYEOGFITDPVV 120
QY 121 LSPKDRYRVFEAKARHGFEGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCFLKEIMT 180
DB 121 LSPSHTVGVDVLEAKIQHGFSGIPITATGTMGSKLVGIWTSRDIDFLAKRDHTTLLSEVMT 180
QY 181 KREDLVVAPRSITLKEANEILORSKKGKLPVINEDELVAIARTDLAKNRDYPLASKDA 240
DB 181 PRVELVVAPAGVTLKEANEILORSKKGKLPVINDQDELVAIARTDLAKNRDYPLASKDS 240
QY 241 KKQLLCGAIGTHEDDKYRLDLAQAQGVNVVLDSSQGSNIFQIMTIRYIKDKYPNLOVI 300
DB 241 HKQLLCGAAGVTRDDKYRLDLTQAQADVIVHSSQGSNSYQIAMVIRYIKOKYPHLOVI 300
QY 301 GGNVYTAQAQAKNLIDAGVDALRVGMGSGSICITQEVNACGRPOATAVKYEYARRFGVP 360
DB 301 GGNVYTAQAQAKNLIDAGVDGLRVGMGCGSICITQEVNACGRPOATAVKYAEYARRFGVP 360
QY 361 VIADGCIQNVGHIAKALALGASTVMGSLAATTEAPGEYFSDGIRLKKYRGMGLDAM 420
||||||| |||: |||||||||||||||||||||||||||||||: |||||: |||||

DB 361 VIADGCIQTVGHVVKALALGASTVMGSLAATTEAPGEYFSDGVRLLKKYRGISLDAM 420
QY 421 DKHLSSQNRYSFSEADKIKVAQGVSCAVQDKSIHKFVPPYLIAGIOHSCODIGAKSLTOVR 480
DB 421 EKSSSSQKRYFSECDKVKIAQGVSGSIQDKGSIQKFPVPLIAGIOHCODIGAQSLSVLR 480
QY 481 AMYSGELKFEKRTSSAQVEGVGSHLSYEKRLF 514
DB 481 SMMYSGELKFEKRTMSAQIEGVGHLSHSEKRLY 514
: ||||||| ||||| |||: ||||| |||||||:

RESULT 6
IMDH_DROME
ID IMDH_DROME STANDARD; PRT; 537 AA.
AC Q07152; Q26455; Q9W2R8;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD) (Raspberry protein).
GN RAS OR CG1799.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Nash D., Hu S.;
RT "Drosophila inosine monophosphate dehydrogenase is encoded at the
RT raspberry locus."
RL (in) Abstracts of the 35th meeting of the Canadian Federation of
RL Biological Societies, pp.72-72, Victoria (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94259281; PubMed=7911114;
RA Nash D., Hu S., Leonard N.J., Tjong S.Y., Phillips D.;
RT "The raspberry locus of Drosophila melanogaster includes an inosine
RT monophosphate dehydrogenase like coding sequence."
RL Genome 37:333-344(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=94114565; PubMed=7904480;
RA Sifri C.D., Wilson K., Smolik S., Forte M., Ullman B.;
RT "Cloning and sequence analysis of a Drosophila melanogaster cDNA
RT encoding IMP dehydrogenase."
RL Biochim. Biophys. Acta 1217:103-106(1994).
RN [4]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=96069715; PubMed=7476879;
RA Slee R., Bownes M.;
RT "The raspberry locus encodes Drosophila inosine monophosphate
RT dehydrogenase."
RL Mol. Gen. Genet. 248:755-766(1995).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Betman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -I- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH.
CC -I- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -I- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -I- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -I- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL: L14847; AAA21831.1; -.
DR EMBL: L22608; AAA16839.1; -.
DR EMBL: S80430; AAB35628.1; -.
DR EMBL: AE003451; AAF46622.1; -.
DR HSSP: P12268; 1B3O.
DR FlyBase: FBgn0003204; ras.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMPDH/GMPrtase.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR TIGRFAMs: TIGR01302; IMP_dehydrog; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT DOMAIN 134 189 CBS 1.
FT 198 251 CBS 2.
FT BINDING 350 350 IMP (BY SIMILARITY).
FT CONFLICT 38 38 D -> V (IN REF. 4).
FT CONFLICT 53 53 T -> P (IN REF. 4).
FT CONFLICT 99 102 EMAI -> RCH (IN REF. 4).
FT CONFLICT 184 184 D -> A (IN REF. 4).
FT CONFLICT 194 194 V -> S (IN REF. 4).
FT CONFLICT 216 217 AN -> EH (IN REF. 4).
FT CONFLICT 226 229 GLKP -> ATA (IN REF. 4).
FT CONFLICT 244 244 T -> A (IN REF. 4).
FT CONFLICT 261 262 KQ -> TR (IN REF. 4).
FT CONFLICT 265 266 VG -> CP (IN REF. 4).
FT CONFLICT 277 278 AR -> GCRA (IN REF. 4).

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[illegible]

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DR EMBL: 246729; CAA86719.1; -
DR HSSP: P12268; 1B3O. -
DR SGD: S0004520; IMD4.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMPdh/GMPrtase.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR TIGRFAMS: TIGR01302; IMP_dehydrog; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 120 175 CBS 1.
FT DOMAIN 183 235 CBS 2.
FT BINDING 336 336 IMP (POTENTIAL).
SQ SEQUENCE 524 AA; 56394 MW; A73D1E4EFE8AEAD9 CRC64

Query Match 61.5%; Score 1610.5; DB 1; Length 524;
Best Local Similarity 61.8%; Pred. No. 1.3e-101;
Matches 316; Conservative 82; Mismatches 102; Indels 11; Gaps 5;

QY 11 SYVPDDGLTAQLFN--CGDGLTYNDFLLPGYIDFTADQVDLTSAITKKITLKTPLVSS 68
Db 17 TYSSKDGLSVQELMDSTTRGILTYNDFLLPGLVNFPSASVSLQTKLTKKITLNTPFVSS 76
QY 69 PMDTVTEAGMATAMALTGIGFIHNCTPEFOANEVRKVKYEOGFTTPVLSPKDRVR 128
Db 77 PMDTVTEADMAIYMALLGIGFIHNCTPKEOASMKVKMFENGFINSPVISPTTVG 136
QY 129 DVEFAKARHGFCGIPITDGRMGSRVLGIISSRIDIDFLKEEHDCFLEIMTKREDLVVA 188
Db 137 EVKVMKRKFGSGFPVTEDEKCPGKGLVLTSTRDIQFL--EDDSLVSIVMTKNP--VTG 192
QY 189 PRSTLTKEANEILQRSKKGLPIVNEDELVAIARTDLKKNRDYPLASKDA-KKQLLCG 247
Db 193 IKGITLKEGNEILKOTKKGLLIVDNGNLVSMLSRADLMKNQNYPLASKSATTKQLLCG 252
QY 248 AAICTHEDDKYRLDLAAGVDVVLDSQGSNIFQINMIKYIKDKYPTLQVIGGNVTA 307
Db 253 AAICTIEADKERLRLLEAGLDVILDSQGSNSVFQINMIKIKETFPLEIAGNVATR 312
QY 308 AQAKNLIDAGVDALRVGMSGSCICITQEVLAGCRPOATAVYKVEYARAFGVPIADGGI 367
Db 313 EQAANLIAAGADGLRIGMSGSCICITQEVMACGRPOGTAVYNVCQFANAFGVPCMADGGV 372
QY 368 QNVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM----DKH 423
Db 373 QNTGHTTKALALGSSVTMMGMLAGTTESPEGEYFYKDKRLKAYRGMGSLDAMQKTGKNG 432
QY 424 LSSQNRIFYSEADKIKVAQGVSAVQDKGSIHKFVYPYLLAGIQHSCQDIYAKSLTQVRAMM 483
Db 433 NASTSRIFYSESDSVLAQGVSAVVDKGSIKKFIPLYLNGLOHSCQDIYCESLTSLKENV 492
QY 484 YSGELKFEKRTSSAQVEGCVHSLHSEKRLF 514
Db 493 QNGEYRFEFRTASAOLEGVHNLHSEKRLY 523

RESULT 8
IMD3_YEAST STANDARD; PRT; 523 AA.
AC P50095;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase IMD3 (EC 1.1.1.205)
DE (IMP dehydrogenase) (IMPDH) (IMPD).
GN IMD3 OR YLR432W OR L9753.4.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich A., Trevasakis E., Vignati D.,
RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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DR EMBL: U21094; AAB67516.1; -
DR HSSP: P12268; 1B3O.
DR SGD: S0004424; IMD3.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMPDH_GMPrtase.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR TIGRFAMS: TIGR01302; IMP_dehydrog; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 56584 MW; A0C84C22527AAEA6 CRC64;

Query Match 61.4%; Score 1607.5; DB 1; Length 523;
Best Local Similarity 62.2%; Pred. No. 2.1e-101;
Matches 314; Conservative 81; Mismatches 99; Indels 11; Gaps 5;

QY 16 DGLTAQQLFN--CGDGLTYNDFLLPGYIDFTADQVDLTSAITKKITLKTPLVSSPMDTV 73
Db 21 DGLSVQELMDSKTRGGLTYNDFLLPGLVDFPSSSEVSLQTKRITLNTLTPFVSSPMDTV 80
QY 74 TEAGMATAMALTGIGFIHNCTPEFOANEVRKVKYEOGFTTDPVLSPKDRVDFEA 133
Db 81 TESEMAIFMALLGIGFIHNCTPEDQADMVRRVKNYENGFINNPVISPTTVGEAKSM 140
QY 134 KARHGPCGIPITDGRMGSRVLGIISSRIDIDFLKEEHDCFLEIMTKREDLVVAPRST 193
Db 141 KERFGSGFPVTEDEKRNKGLMGLVTSRDIQFV--EDNSLLVQDVMYTKNP--VTGAQGIT 196
QY 194 LKEANETLQRSKKGLPIVNEDELVAIARTDLKKNRDYPLASKDA-KKQLLCGAATGT 252
Db 197 LSEGNETLKKIKKGLLIVDNGNLVSMLSRTDLMKNQNYPLASKSATTKQLLCGAATGT 256

QY	253	HEDDKYRLDLLAÖGVDVNVLLDSÖGNSIFÖINMIKYYIKDKYPNLÖVITGNNVTAÄÖAKN	312
		: : : : : : :	
Db	257	IDADKERLRLVEAGLDVNLDSÖGNSIFÖLNMIKWIKETFPDLEITAGNVATREQAAN	316
QY	313	LIDAGVDALRVGMGSICIIÖEVLACGRPOATAVYKVEYARREGVPYIADGCIÖNVGH	372
		: : : : :	
Db	317	LIAAGADGLRIGMGSGSICITÖEYMACGRPOGTAVYNNVCEFANÖFGIPCMA DGGVÖNIGH	376
QY	373	IAKALALGASTVMMGSLAATTEAPGEYFEFSDGIRLKKYRGMSILDAMD---KHLSSÖN	428
		: :	
Db	377	ITKALALGSSTVMMGMLAGTTESPGEYFÖYÖDGKRLKAYRGMGSIDAMÖKTGTKNASTS	436
QY	429	RYFSEADKIKVAÖGVSGAVÖDKGSIHKFVPLYLAGIÖHSCÖDIGAKSLTÖYRAMMYSGEL	488
		:	
Db	437	RYFSES DSVLVAÖGVSGAVVDKGSITKFIPLYNLGÖHSCÖDIGYKSLTLKENVÖSGKV	496
QY	489	KFEKRTSSAÖVEGGVHSLHSEKRL	513
		: : :	
Db	497	RFEERTASAOLEGGVHNLHSEKRL	521

```

RESULT 9
IMH3_CANAL
ID IMH3_CANAL STANDARD; PRT: 521 AA.
AC 000086;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN IMH3.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS;
RX MEDLINE=97234646; Pubmed=9079920;
RA Koehler G.A., White T.C., Agabian N.;
RT "Overexpression of a cloned IMP dehydrogenase gene of Candida
RT albicans confers resistance to the specific inhibitor mycophenolic
RT acid.";
RL J. Bacteriol. 179:2331-2338(1997).
CC -1- FUNCTION: ESSENTIAL ENZYME IN THE DE NOVO BIOSYNTHESIS OF GMP,
CC CATALYSING THE NAD-DEPENDENT OXIDATION OF IMP TO XMP.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT EQUAL LEVELS IN THE YEAST OR
CC HYPHAL FORM.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U85049; AAB51509.1; -.
DR HSSP: P12268; 1B3O.
DR COMPLYEAST-2DPAGE; 000086; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPDH/GMPrtase.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.

```

DR	TIGRFAMS, TIGR01302; IMP_dehydrog; 1.
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW	Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW	CBS domain.
FT	DOMAIN 117 172 CBS 1.
FT	DOMAIN 180 232 CBS 2.
FT	BINDING 333 IMP (POTENTIAL).
SC	SEQUENCE 521 AA; 56239 MW; 5F1E52611B1E1418 CRC64;

Query Match	61.38;	Score 1605.5;	DB 1;	Length 521;
Best Local Similarity	63.58;	Pred. No. 2.8e-101;		
Matches 329;	Conservative 68;	Mismatches 106;	Indels 15;	Gaps 6

```

0y      7 SGGTSTYVPD-----DGLTAQQLFNCGD--GLTYNDFLLPGYIDFTADQVDLTSA LTKKIT 600
      |   | | | : : : : : | | | | | | | | | | | | | | | | | | | | | | |
Db      6 SKATSYLKDYPPKRDGLSVKELIDSTNFGGLTYNDFLLPGLINFPSSAVSL ETKLTKKIT 650

```

QY 61 LKIPLVSSPMDVTVEAGMAIAMALTGGIGFIHNNCTPEQANEVRKVKKYEQGFITDPVV 120
 66 LKSPFVSSPMDVTVEENMAIHMALIGIGIIHNNCTSEQAEVVRKVKKYENGFINDPVV 125

QY 121 LSPKDRVDFEAKARHGFCGIPITDTGRMGSRLVGISSRDIDFLKEEHDCPLEIIMT 180
::: | : | : | | : : | : : | : : | : : | : : | : : | : : | : :
Db 126 ISPEVLTVGEVKMKGEVLGFTSPFVTENGKVGGKLVIITSRDIQ--HEDNKSPPVEVMYT 183

QY 181 KREDLVAPRSITLKEANEILÖRKRKKGLPIVNEDEDLVALIARTDCLKNRDPPLASKD- 239
+ + + + : : : : + + + + + : : : : + + + + + + + +
Db 184 K-DLVGKKGISLTGDGNELLRRSKKGLPIVDAEGLVSLISRTDLOKNODYPNASKSF 241

QY 240 AKKQLLGAIGTHEDDKYRLDLAQAQVDVVLDDSSQGNSTFQINMIKYIKDKYPNLQY 299
 | | | | | : : : | : : | | | | | : : : | | | | |
Db 242 HSKOLLGGAIGTIDADRERLDKIYEAGLDVVLLDSSNGSSFOLNMKIWIKEKYPELOV 301

QY 300 IGGNVVTAQAOKNLIDAGVDALRVGMSGSCICIQEVLACGRPOATAVYKVYEYARREGV 359
| | | | | | : | | | | | | | | | | | | | | | | : | | |
Db 302 IAGNVVTRBOAALLIEAGADALRIIGMSGSCICTOEFVMCGRPOGTAVYGTEFANEFGV 361

QY 360 PVIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEFFFSDGIRLKKRYRGMGSIDA 419
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 362 PCTADGGIGNIGHTTKALAI GASTVMGGLAGTAFTPGDVEYRDGRI KTYRGMGSIDA 421

OY 420 MDKHLSSQN---RYFSEADKIKAQGVSGAVODKGSIHKFPVPILAGIQHSCDGTAKS 475
| : : | ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Dh 422 MOONTNNAASTSPYEFADKVLVAOAGVGSGVDKGSITKEFDYT YNGI OHST ADIGTFS 481

QY 476 LTQVRAMYSGEILFEKRTSSAQVEGVSHLSYEKRL 513
:
DB 482 TDFEIRNDNGCFREPERPTASAOFFEGCHGT HSYEKPT 510

RESULT 10

ID	IMD2_YEAST	STANDARD;	PRT;	523	AA
AC	P38697;				
DT	01-FEB-1995	(Rel. 31, Created)			
PT	01-FEB-1995	(Rel. 31, First Sequence Updated)			

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase IMD2 (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
DE
DE
DE

05 *Saccharomyces cerevisiae* (Baker's yeast).
0C Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
0C Saccharomycetales; Saccharomycetaceae; Saccharomyces.

RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=S288C / AB972;	

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,

RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA

RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VII.1";
RL Science 265:2077-2082(1994).
CC -i- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -i- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS;
CC -i- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -i- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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CC or send an email to license@isb-sib.ch).

DR EMBL; U00029; AAB69728.1; -
DR PIR; S48997; S48997.
DR HSSP; P12268; 1B3O.
DR SGD; S0001259; IMD2.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPdh/GMPcase.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 56530 MW; 7CA3EC11238906B9 CRC64

Query Match 60.7%; Score 1589.5; DB 1; Length 523;
Best local Similarity 61.2%; Pred. No. 3.4e-100;
Matches 309; Conservative 84; Mismatches 101; Indels 11; Gaps 5;

QY 16 DGLTAQQLFN--CGDGLTYNDLFLIPGYIDFTADQVDLTSLTKITLTPLVSSPMDTV 73
Db 21 DGLSVDELMSKIRGLTYNDLFLIPGLVDFASSVSLQTKLTRNTLTIPLVSSPMDTV 80
QY 74 TEAGMALAMALTGIGIFHHNCTPEFOANEVRKVKVEOGFITDPVYLSPKDRVRDVEEA 133
Db 81 TESEMAFMAALLGGIGIFHHNCTPEOQADMVRVKVKNYENGFINNPVHSPTTVGEAKSM 140
QY 134 KARHFGCIGIPITDTGRMSRLVGIISRDIDFLKEEHDFLEETMTKGEDLVVAPRSIT 193
Db 141 KEKYGFAGFPVTTDGKRNKAKLVGVTSRDIQFV--EDNSLLVQDVMTKIP--VTGAQGIT 196
QY 194 LKEANEILQRSKKKGLPIVNEDELVAIIARTDLKKNRDYPLASKDAK KOLLGGAIGT 252
Db 197 LSEGNELKKIKKGRLLVDEKGNLVSMLSRDTLKNQNYPLASKSAN KOLLGASIGT 256
QY 253 HEDDKYRLDLLAQAQVDVVVLDSSGNSIFOINMIKYIKDKYPNIQVTEGNVNTAAQAKN 312
Db 257 MDADKERLLLVKAGLDVILDSGNSIFELNMLKWKVESFEGLEVHAGNVVTRQQAAN 316
QY 313 LIDAGVDALRVGMGSGSICITQEVLAACGRQATAVYKVEYARFGVPTIADGIQNVGH 372
Db 317 LIAAGADGLRIGMGTSICITQEVMAACGRPGTAVYVNCVFANQFCVPMADGCVQNIIGH 376
QY 373 IAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGLDAMD---KHLSSQN 428
Db 377 ITKALALGSSTVMMGMGLAGTSEPGYEYFYQDGKRLKAYRGMGSIDAMDKTGTKGNASTS 436
QY 429 RYFSEADKIKVAQGVSGAVQDKSGTHKFVRYLLIAGIQHSCQDICAQSLQVRAMMYSGEL 488

Db 437 RYFSESDSVLVAQGVSGAVVDKSGTIRKPIPYLYNGLQHSQCQDIGCRSLTLKNNVQRKV 496
QY 489 KFEKRTSSAOVEGGVHSLHSYEKRL 513
Db 497 RFEFRTASAOLEGVHNLHSYEKRL 521

RESULT 11
IMDH_SCHPO
ID IMDH_SCHPO STANDARD; PRT; 524 AA.
AC 014344; Q9P3X8.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUA1 OR SPBC2F12.14C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [2]
RP SEQUENCE OF 378-524 FROM N.A.
RC STRAIN=972;
RA karaer S., Topal Sarykaya A., Temizkan G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -i- FUNCTION: Essential enzyme in the de novo biosynthesis of GMP,
CC catalyzing the NAD-dependent oxidation of IMP to XMP.
CC -i- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -i- PATHWAY: First reaction unique to GMP biosynthesis.
CC -i- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP
CC REDUCTASE.
CC -i- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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Db 356 SGKNGDNAASRYEGEADTIRVAQGVSGSVIDKGS�HVVPYLRITGQHSLQDIGVNL 415

QY 477 TQVRAMMYSGELKFEKRTSSAQVEGCVHSLHSEKRLF 514

Db 416 TELRKQVKEKNIRFEFRTVASQLEGNVHGLDSYQKKLW 453

RESULT 13

IMDH_TRYBB STANDARD; PRT; 512 AA.

AC P50098;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP dehydrogenase) (IMPDH) (IMPD).

OS Trypanosoma brucei brucei.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

OX NCBI_TaxID=5702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EATRO 164 / ISTAT 1.7;

RX MEDLINE=95050714; PubMed=7961861;

RA Wilson K., Berens R.L., Sifri C.D., Ullman B.;

RT "Amplification of the inosinate dehydrogenase gene in Trypanosoma brucei gambiense due to an increase in chromosome copy number.";

RL J. Biol. Chem. 269:28979-28987(1994).

CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION OF CELL GROWTH.

CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O = xanthosine 5'-phosphate + NADH.

CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.

CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP REDUCTASE.

CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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CC -----

DR EMBL; M97794; AAB46420.1; -.

DR HSSP; P12268; 1B3O.

DR InterPro; IPR000644; CBS_domain.

DR InterPro; IPR003009; FMN_enzyme.

DR InterPro; IPR001093; IMPdh/GMPase.

DR Pfam; PF00478; IMPDH_C; 1.

DR Pfam; PF00571; CBS; 2.

DR Pfam; PF01574; IMPDH_N; 1.

DR SMART; SM00116; CBS; 2.

DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.

DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.

KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat; CBS domain.

FT DOMAIN 108 163 CBS 1.

FT DOMAIN 170 226 CBS 2.

FT BINDING 325 325 IMP (POTENTIAL).

SEQUENCE 512 AA; 55708 MW; 1A86C46AE6445045 CRC64

Query Match 52.9%; Score 1385.5; DB 1; Length 512;

Best Local Similarity 54.1%; Pred. No. 2e-86;

Matches 270; Conservative 91; Mismatches 135; Indels 3; Gaps 2;

QY 16 DGLTAQQLFNGDGLTYNDFLLPGYIDFTADQVDLTSLTKRITLKT LVSSPMDVTVE 75

Db 13 DGTAAEELFS-QDGLSFNDFIILPGFIDFSSKVNVSQGFYTKNILLHL LVSSPMDVTVE 71

QY 76 AGMALMALTGIGIFIHNCPTFEQANEVRKVKYEQGFITDPVYLSPTDRVDRVFEAKA 135

Db 72 SSMARAMALMGIGIVIHNNCTVEQQAQARVRSVKLYRNGFIMKPKSVSPDVPVSTIRNIKS 131

QY 136 RHFGCIPITDTGRMGSRVLGIISSRPIDFLKEEHDCLFEIMTKREDLVAPRSITLK 195

Db 132 EKGISGLVITGGKYDGKLLGIVCTKIDFVKDASAP--VSQYMTREMMTVERYPKLE 189

QY 196 EANEILQSRKKGLPIVNEDELVAIARTDLKKNRDYPLASKDAKKOLLGAAIGTHED 255

Db 190 EAMDVLNRSRHGYLPVLNDKDEVVCLCSRDAVARDYPNSSLDRNGHLLCAAATSTREA 249

QY 256 DKYRLDLAQAQVDVVLDDSSQNSIFQINMIKYIKDKYPNLQVIGCNVVTAAQAKNLID 315

Db 250 DKGRVAALSEAGIDVLVLDDSSQNTIYQVSFIRWVKKTYPHLEVVAGNVVTDQAKNLID 309

QY 316 AGVDALRVGMSGSCITIOEVLACGRPOATAVYKVEYARARFGVPVIADGCIQNVGHIAK 375

Db 310 AGADSLRIGMSGSCITIOEVLACGRPOATAIYKVARYAASRGVPCVADGGLRNVGDVCK 369

QY 376 ALALGASTVMGSLLAATTEAPGEYFSDGIRLKKYRGMGSLDAMDKHLSSQNRYFSEAD 435

Db 370 ALAVGANVAMGSMIAGTSETPGEYFFKGMRLKGYRGMGSLDAMDLOGRESGKRYLSENE 429

QY 436 KIKVAQGVSAVQDKGSIHKFVPLYIAGIQHSCODIGAKSLTQVRAMMYSGELKFEKRTS 495

Db 430 TLQVAQGVAGAVLDKGSVLLKLAYIHKGLOQSAODIGEVSFDAIREKRYEGQVLFNRRTL 489

QY 496 SAQVEGCVHSLHSEKRLF 514

Db 490 TAOSEGAVHSLHSEKRLF 508

RESULT 14

IMDH_LEIDO STANDARD; PRT; 514 AA.

AC P21620;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP dehydrogenase) (IMPDH) (IMPD).

OS Leishmania donovani.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5661;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91107664; PubMed=1671039;

RA Wilson K.E., Collart F.R., Huberman E., Stringer J.R., Ullman B.;

RT "Amplification and molecular cloning of the IMP dehydrogenase gene of Leishmania donovani.";

RL J. Biol. Chem. 266:1665-1671(1991).

CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION OF CELL GROWTH.

CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O = xanthosine 5'-phosphate + NADH.

CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.

CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP REDUCTASE.

CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.

CC -----

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CC -----

DR EMBL; M55667; AAA29253.1; -.

DR PIR; A38668; A38668.

DR HSSP; P12268; 1B3O.

DR InterPro; IPR000644; CBS_domain.

DR InterPro; IPR003009; FMN_enzyme.

DR InterPro; IPR001093; IMPdh/GMPrtase.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CBS domain.
FT DOMAIN 110 165 CBS 1.
FT DOMAIN 172 228 CBS 2.
FT BINDING 327 327 IMP (POTENTIAL).
SQ SEQUENCE 514 AA; 55551 MW; E251FCC1362D60E5 CRC64;

Query Match 52.4%; Score 1371.5; DB 1; Length 514;
Best local Similarity 53.7%; Pred. No. 1.8e-85;
Matches 268; Conservative 83; Mismatches 145; Indels 3; Gaps 2;

QY 16 DGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSALTKKITLKTPLVSSPMDTVE 75
DB 15 DGTAEELFR-GDGLTYNDFIILPGFIDGADAVNISGQFTKRIRLHPIVSSPMDTITE 73

QY 76 AGMAIAMLTGIGIFIHNCPTPEFOANEVRKKYEQGFITDPVVLSPKDRVDFEAKA 135
DB 74 NEMAKTMALMGVGLHNNCTVERQVEYKSVKAYRNGFISKPKSVPPNTPISNIIRIKE 133

QY 136 RHGFCGIPITDTGRMGSRVLGVISSRDIDFLKEEHCFLFEIMTKREDLVVAPRSITLK 195
DB 134 EKGISGLVTENGDPHGKLLGIVCTKDIDYVKNK--DTPVSAVMTREKMTVERAPIQLE 191

QY 196 EANEILORSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDAKKQLLCGAATGHED 255
DB 192 EAMDVLNRSRYGLPIVNEDEVNLCSDRDVAVRADYPHSTLDKSGRLICAATSTRPE 251

QY 256 DKYRLDLAQAGVDVVLDDSSQGSNIFQIINMIKYIKDKYPNLQVIGNVYTAQAKNLID 315
DB 252 DKRRVAALADVGVDVLVLDSSQGNITVQIAFIKWKSTYPHLEVAGNVYTQDAQKNLID 311

QY 316 AGVDALRVGMSGSGICIIQEVLAGCRPQATVAVKVEYARRFVGPVIADGCIQNVGHIAK 375
DB 312 AGADGIRIGMSGSGICITQEVLAGCRPQGTAVYKVAQYCASRGVPCPTADGGLRQVGDICK 371

QY 376 ALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHSSQNRYFSEAD 435
DB 372 ALAIGANCAMLGMLSGTTEPGEYFFKGVRLKYYRGMGSLAAMSQGESGKRYLSENE 431

QY 436 KIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAKSLTQVRAMYSGELKFEKRTS 495
DB 432 AVQVAQGVSGNVYDKGSAKLIAYVSKLQOOSAQDIGEISFDAIREKMYAGQVLFSSRRSP 491

QY 496 SAOEGGVHSLHSYEKRLF 514
DB 492 TAQEGGVHSLHSYEKRLF 510

RESULT 15
IMH2_ARATH
ID IMH2_ARATH STANDARD; PRT; 502 AA.
AC Q9SA34;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP dehydrogenase) (IMPDH) (IMPD).
GN ATG16350 OR F309.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;

RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Iam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana."
RT Nature 408:816-820(2000).
CC -I- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -I- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -I- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP REDUCTASE.
CC -I- SIMILARITY: CONTAINS 1 CBS DOMAIN.

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CC or send an email to license@isb-sib.ch).

DR EMBL; AC006341; AAD34687.1; -.
DR HSSP; P12268; 1B3O.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMPdh/GMPrtase.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR TIGRFAMS; TIGR01302; IMP_dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT DOMAIN 167 219 CBS.
FT BINDING 321 321 IMP (POTENTIAL).
SQ SEQUENCE 502 AA; 54051 MW; FB87D84160818310 CRC64;

Query Match 44.1%; Score 1155; DB 1; Length 502;
Best local Similarity 47.4%; Pred. No. 7.6e-71;
Matches 239; Conservative 93; Mismatches 162; Indels 10; Gaps 6;

QY 15 DDGLTAQQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSALTKKITLKTPLVSSPMDTVE 74
DB 5 EDGFSAEKLFSSQGYSTYTDVIFLPHFIDFSTDAVSLSTRLSKRVPLSIPCVASPMDTVS 64

QY 75 EAGMAIAMLTGIGIFIHNCPTPEFOANEVRKKYEQGFITDPVVLSPKDRVDFEAK 134
DB 65 ESHMAAAMALGIGIVHYNCIDITQASVIRHAKSLQVPIASDAVFKCPHQIGSV-DDF 123

QY 135 ARHFGCIPITDTGRMGSRVLGVISSRDIDFLKEEHCFLFEIMTKREDL-VVAPRSIT 193
DB 124 GPSSF--VFVSQTGTLTLPKLLGVSKSEWSSMKDDQKEVKIYDWMKSCENKDYVVPWDID 181

QY 194 LKEANEILORSKKGKLPVNEDELVAIARTDLKKNRDY---LASKDAKKQLLCGAAI 250
DB 182 LDKIEAVLEDKQKG-FVLEKEGETVNVVTKDVERVKGYPKLGSSTVGADKKMMVGAAI 240

QY 251 GTHEDDKYRLDLAQAGVDVVLDDSSQGSNIFQIINMIKYIKDKYPNLQVIGNVYTAQA 310
DB 241 GTRESDKERLEHLVKAGANVVVLDDSSQGSNITYLEMIKYYKNTYPELADVGVGNVVTMYQA 300

Thu Feb 13 13:18:50 2003

us-09-846-637c-4.rsp

Page 13

[illegible]

Search completed: February 13, 2003, 04:51:16
Job time : 44 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 04:36:17 ; Search time 63 Seconds
(without alignments)
932.323 Million cell updates/sec

Title: US-09-846-637C-4
Perfect score: 2619
Sequence: 1 MADVLIISGTSYVPDDGLTA.....SSAQVEGVHSLHSEYKRLF 514

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2595	99.1	514	1	A31997	IMP dehydrogenase
2	2559	97.7	514	1	B31997	IMP dehydrogenase
3	2555	97.6	514	1	JT0565	IMP dehydrogenase
4	2222	84.8	514	1	A35566	IMP dehydrogenase
5	1764.5	67.4	537	1	S41064	IMP dehydrogenase
6	1635.5	62.4	537	1	S55508	IMP dehydrogenase
7	1610.5	61.5	524	1	S50890	IMP dehydrogenase
8	1607.5	61.4	523	1	S59402	IMP dehydrogenase
9	1589.5	60.7	523	1	S48997	IMP dehydrogenase
10	1473.5	56.3	524	1	T40127	IMP dehydrogenase
11	1385.5	52.9	512	1	A55407	IMP dehydrogenase
12	1363.5	52.1	514	1	A38668	IMP dehydrogenase
13	1324.5	50.6	499	1	T32709	IMP dehydrogenase
14	1155	44.1	502	2	F86298	IMP dehydrogenase
15	1106.5	42.2	503	1	JC4999	IMP dehydrogenase
16	1043.5	39.8	403	2	S53477	IMP dehydrogenase
17	966.5	36.9	485	2	G81308	IMP dehydrogenase
18	958	36.6	485	2	D97232	IMP dehydrogenase
19	952	36.3	490	1	H70473	IMP dehydrogenase
20	922	35.2	485	2	D83652	IMP dehydrogenase
21	914	34.9	487	2	F81906	IMP dehydrogenase
22	911	34.8	487	1	H81109	IMP dehydrogenase
23	910	34.7	485	2	B82558	IMP dehydrogenase
24	904.5	34.5	482	2	C72264	IMP dehydrogenase
25	886.5	33.8	488	1	DEBSMP	IMP dehydrogenase
26	885	33.8	509	2	JC7305	IMP dehydrogenase
27	875	33.4	489	2	H83173	IMP dehydrogenase
28	860	32.8	488	2	G89805	IMP dehydrogenase
29	858.5	32.8	499	2	AC3621	IMP dehydrogenase

30	857.5	32.7	488	1	S23226	IMP dehydrogenase
31	855.5	32.7	500	1	F75342	IMP dehydrogenase
32	849.5	32.4	529	1	H70736	IMP dehydrogenase
33	846.5	32.3	488	2	AE1419	IMP dehydrogenase
34	846.5	32.3	488	2	AF1794	IMP dehydrogenase
35	846	32.3	489	2	C82282	IMP dehydrogenase
36	839.5	32.1	529	1	S72823	IMP dehydrogenase
37	837	32.1	488	1	DEECIP	IMP dehydrogenase
38	837	32.C	488	2	B91050	IMP dehydrogenase
39	837	32.C	488	2	G85894	IMP dehydrogenase
40	836	31.9	488	1	H64055	IMP dehydrogenase
41	832.5	31.8	493	2	D86652	IMP dehydrogenase
42	827.5	31.6	521	1	T17196	IMP dehydrogenase
43	827	31.6	487	2	AG0349	IMP dehydrogenase
44	819.5	31.3	487	2	H87449	IMP dehydrogenase
45	818	31.2	490	2	AE0820	IMP dehydrogenase

ALIGNMENTS

RESULT 1

A31997

IMP dehydrogenase (EC 1.1.1.205) II - human

N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH) type II
C:Species: Homo sapiens (man)

C:Date: 21-May-1990 #sequence_revision 22-May-1998 #text_change 16-Jul-1999
C:Accession: I52303; I54184; A92676; B35566; A31997; A94550

R:Giesne, D.A.; Huberman, E.

Biochem. Biophys. Res. Commun. 205, 537-544, 1994

A:Title: Cloning and sequence of the human type II IMP dehydrogenase gene.

A:Reference number: I52303; MUID:95091778; PMID:7999076

A:Accession: I52303

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-514 <GLE1>

A:Cross-references: GB:L33842; NID:g602457; PIDN:AAA67054.1; PID:g602458

R:Giesne, D.A.; Collart, F.R.; Varkony, T.; Drabkin, H.; Huberman, E.

Genomics 16, 274-277, 1993

A:Title: Chromosomal localization and structure of the human type II IMP dehydrogenas

A:Reference number: I54184; MUID:93252398; PMID:8098009

A:Accession: I54184

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 461-514 <GUE2>

A:Cross-references: GB:L08114; NID:g292239; PIDN:AAA36113.1; PID:g292240

R:Collart, F.R.; Huberman, E.

J. Biol. Chem. 263, 15769-15772, 1988

A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-mo

A:Reference number: A92676; MUID:89008491; PMID:2902093

A:Accession: A92676

A:Molecule type: mRNA

A:Residues: 1-189, 'Re', 192-514 <COL>

A:Cross-references: GB:J04208; NID:g186391; PIDN:AAA36112.1; PID:g307066

A:Note: submitted to the Protein Sequence Database, November 1989

R:Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.

J. Biol. Chem. 265, 5292-5295, 1990

A:Title: Two distinct cDNAs for human IMP dehydrogenase.

A:Reference number: A35566; MUID:90203022; PMID:1969416

A:Accession: B35566

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-514 <NAT>

C:Comment: mRNA for IMP dehydrogenase I (see PIR:A35566) predominated in normal leuko

C:Genetics:

A:Gene: GDB:IMPDH2

A:Cross-references: GDB:128086; OMIM:146691

A:Map position: 3p24.2-3p21.2

A:Introns: 33/2; 49/3; 83/3; 108/3; 177/3; 207/1; 274/1; 304/1; 336/1; 432/2; 480/2;

C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu

A:pathway: purine nucleotide biosynthesis

C:superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo

C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match 99.1%; Score 2595; DB 1; Length 514;
Best Local Similarity 99.2%; Pred. No. 3.2e-160;
Matches 510; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADYLLISGGSYVPDDGLTAAQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
Db 1 MADYLLISGGSYVPDDGLTAAQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKYEQGFITDPVV 120
Db 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKYEQGFITDPVV 120
QY 121 LSPKDRVDFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLFEIMT 180
Db 121 LSPKDRVDFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLFEIMT 180
QY 181 KREDLVVAPRSITLKEANEILORSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVVAPAGITLKEANEILORSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
QY 241 KKQLLCGAAGTHEDDKYRLDLLAQAGVDVYVLDSSQGSNIFQINMIKIKDKYPNLQVI 300
Db 241 KKQLLCGAAGTHEDDKYRLDLLAQAGVDVYVLDSSQGSNIFQINMIKIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPQATAVYKVEYARREGVP 360
Db 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPQATAVYKVEYARREGVP 360
QY 361 VIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRFFEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAASLTQVR 480
Db 421 DKHLSSQNRFFEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAASLTQVR 480
QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514
Db 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514

RESULT 2
B31997
IMP dehydrogenase (EC 1.1.1.205) - Chinese hamster
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: B31997
R:Collart, F.R.; Huberman, E.
J. Biol. Chem. 263, 15769-15772, 1988
A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-monophosphate dehydrogenase
A:Reference number: A92676; MUID:89008491; PMID:2902093
A:Accession: B31997
A:Molecule type: mRNA
A:Residues: 1-514 <COL>
A:Cross-references: GB:J04209; NID:g191119; PIDN:AAA36993.1; PID:g304517
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match 97.7%; Score 2559; DB 1; Length 514;
Best Local Similarity 98.1%; Pred. No. 6.9e-158;
Matches 504; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MADYLLISGGSYVPDDGLTAAQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
Db 1 MADYLLISGGSYVPDDGLTAAQLFNCGDGLTYNDFLLPGYIDFTADQVDLTSAITKKIT 60
QY 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKYEQGFITDPVV 120
Db 61 LKTPLVSSPMDVTVEAGMAIAMALTGGIGFIHNCTPEFOANEVRKVKYEQGFITDPVV 120
QY 121 LSPKDRVDFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLFEIMT 180
Db 121 LSPKDRVDFEAKARHFGCGIPITDTGRMGSRVLGIISSRDIDFLKEEHCFLFEIMT 180
QY 181 KREDLVVAPRSITLKEANEILORSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
Db 181 KREDLVVAPAGITLKEANEILORSKKGKLPVNEDELVAIARTDLKKNRDYPLASKDA 240
QY 241 KKQLLCGAAGTHEDDKYRLDLLAQAGVDVYVLDSSQGSNIFQINMIKIKDKYPNLQVI 300
Db 241 KKQLLCGAAGTHEDDKYRLDLLAQAGVDVYVLDSSQGSNIFQINMIKIKDKYPNLQVI 300
QY 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPQATAVYKVEYARREGVP 360
Db 301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLAGCRPQATAVYKVEYARREGVP 360
QY 361 VIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
Db 361 VIADGGIONVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMSLDAM 420
QY 421 DKHLSSQNRFFEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAASLTQVR 480
Db 421 DKHLSSQNRFFEADKIKVAQGVSGAVQDKGSIHKFVPLYLAGIQHSCQDIGAASLTQVR 480
QY 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514
Db 481 AMMYSGELKFEKRTSSAQVEGCVHSLHSYEKRLF 514

RESULT 3
JT0565
IMP dehydrogenase (EC 1.1.1.205) - mouse
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: Mus musculus (house mouse)
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: JT0565; A34375; S42724
R:Tiedeman, A.A.; Smith, J.M.
Gene 97, 289-293, 1991
A:Title: Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.
A:Reference number: JT0565; MUID:91153661; PMID:1671845
A:Accession: JT0565
A:Molecule type: mRNA
A:Residues: 1-514 <TIE>
A:Cross-references: GB:M33934; NID:g198393; PIDN:AAA39311.1; PID:g309413
R:Hodges, S.D.; Fung, E.; McKay, D.J.; Renaux, B.S.; Snyder, F.F.
J. Biol. Chem. 264, 18137-18141, 1989
A:Title: Increased activity, amount, and altered kinetic properties of IMP dehydrogenase
A:Reference number: A34375; MUID:90036890; PMID:2572589
A:Accession: A34375
A:Molecule type: protein
A:Residues: 125-134;182-194;289-290;439-449;456-457,'L',459-464,'S',466;475-478 <HOD>
R:Lightfoot, T.; Snyder, F.F.
Biochim. Biophys. Acta 1217, 156-162, 1994
A:Title: Gene amplification and dual point mutations of mouse IMP dehydrogenase associated with the development of the mouse
A:Reference number: S42724; MUID:94153991; PMID:7906545
A:Accession: S42724
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-332,'I',334-350,'Y',352-482,'M',484-514 <LIG>
A:Cross-references: EMBL:M98333; NID:g425157; PIDN:AAA20181.1; PID:g425158

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match		97.6%;	Score 2555;	DB 1;	Length 514;
Best Local Similarity		97.9%;	Pred. No. 1.3e-157;		
Matches 503;		Conservative 4;	Mismatches 7;	Indels 0;	Gaps 0;
Oy	1	MADYLLISGTSYVPDDGLTAQQLFNCGDLTYNDFLLPGYIDFTADGVDLTSALTKKIT	60		
Db	1	MADYLLISGTSYVPDDGLTAQQLFNCGDLTYNDFLLPGYIDFTADGVDLTSALTKKIT	60		
Oy	61	LKTPLVSSPMDVTVEAGMAIAMALTGGIGFIHHNCTPEFOANEVRKVKYEÖGFITDPV	120		
Db	61	LKTPLVSSPMDVTVEAGMAIAMALTGGIGFIHHNCTPEFOANEVRKVKYEÖGFITDPV	120		
Oy	121	LSPKDRVRDVEAKARHGFSGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCEFLIEIMT	180		
Db	121	LSPKDRVRDVEAKARHGFSGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCEFLIEIMT	180		
Oy	181	KREDLVAPRSITLKEANEILÖRSKKGKLPIVENDEDELVAIARTDLKKNRDYPLASKDA	240		
Db	181	KREDLVAPRGVTLKEANEILÖRSKKGKLPIVENDEDELVAIARTDLKKNRDYPLASKDA	240		
Oy	241	KKÖLLCGAIGTHEDDKYRLDLAQAGVDVVLDDSSÖGNSIFÖJINMIKTKDKYPNLÖVI	300		
Db	241	KKÖLLCGAIGTHEDDKYRLDLALAGVDVVLDDSSÖGNSIFÖJINMIKTKDKYPNLÖVI	300		
Oy	301	GGNVTTAAQAKNLIDAGVDALRVGMGSGSICITÖEVLACGRPQATAVYKVEYARRFQVP	360		
Db	301	GGNVTTAAQAKNLIDAGVDALRVGMGSGSICITÖEVLACGRPQATAVYKVEYARRFQVP	360		
Oy	361	VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRKKYRGMSLDAM	420		
Db	361	VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRKKYRGMSLDAM	420		
Oy	421	DKHLSSÖNRYFSEADKIKVAÖGVSGAVODKSGSIHKFVRYLIAIGIÖHSCÖDIGAKSLTÖVR	480		
Db	421	DKHLSSÖNRYFSEADKIKVAÖGVSGAVODKSGSIHKFVRYLIAIGIÖHSCÖDIGAKSLTÖVR	480		
Oy	481	AMMYSGELKFEKRTSSAÖVEGVHSLHSYEKRLF	514		
Db	481	AMTYSGELKFEKRTSSAÖVEGVHSLHSYEKRLF	514		

RESULT 4
A35566
IMP dehydrogenase (EC 1.1.1.205) I - human
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 05-May-2000
C:Accession: A35566
R:Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.
J. Biol. Chem. 265, 5292-5295, 1990
A:Title: Two distinct cDNAs for human IMP dehydrogenase.
A:Reference number: A35566; MUID:90203022; PMID:1969416
A:Accession: A35566
A:Molecule type: mRNA
A:Residues: 1-514 <NAT>
A:Cross-references: GB:J05272; NID:g186393
A:Note: the sequence in GenBank entry HUMIMPH, release 10, (PID:g307067) has 273-Phe, 2
C:Comment: mRNA for IMP dehydrogenase I predominated in normal leukocytes, whereas that
C:Genetics:
A:Gene: GDB:IMPDH1; SMS52608
A:Cross-references: GDB:128085; OMIM:146690

A:Map position: 7q31.3-7q32
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domain: CBS homology <CBS1>
F:184-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match		84.8%;	Score 2222;	DB 1;	Length 514;
Best Local Similarity		83.1%;	Pred. No. 4.2e-136;		
Matches 427;		Conservative 39;	Mismatches 48;	Indels 0;	Gaps 0;
Oy	1	MADYLLISGTSYVPDDGLTAQQLFNCGDLTYNDFLLPGYIDFTADQVDLTSALTKKIT	60		
Db	1	MADYLLISGTSYVPDDGLTAQQLFASADDLTYNDFLLPGYIDFTADQVDLTSALTKKIT	60		
Oy	61	LKTPLVSSPMDVTVEAGMAIAMALTGGIGFIHHNCTPEFOANEVRKVKYEÖGFITDPV	120		
Db	61	LKTPLVSSPMDVTVEADMAIAMALMGIGFIHHNCTPEFOANEVRKVKYEÖGFITDPV	120		
Oy	121	LSPKDRVRDVEAKARHGFSGIPITDTGRMGSRVLGIISSRDIDFLKEEHDCEFLIEIMT	180		
Db	121	LSPHTVGDVLEAKMRHGFSGIPITETGMGSKLVGIVTSRDIDFLAEKDHTLLSEVMT	180		
Oy	181	KREDLVAPRSITLKEANEILÖRSKKGKLPIVENDEDELVAIARTDLKKNRDYPLASKDA	240		
Db	181	PRIELVAPRGVTLKEANEILÖRSKKGKLPINDCDELVAIARTDLKKNRDYPLASKDS	240		
Oy	241	KKÖLLCGAIGTHEDDKYRLDLAQAGVDVVLDDSSÖGNSIFÖJINMIKTKDKYPNLÖVI	300		
Db	241	ÖKÖLLCGAAGCTREDDKYRLDLTAQAGVDVVLDDSSÖGNSVYÖIAMVHYIKÖKYPNLÖVI	300		
Oy	301	GGNVTTAAQAKNLIDAGVDALRVGMGSGSICITÖEVLACGRPQATAVYKVEYARRFQVP	360		
Db	301	GGNVTTAAQAKNLIDAGVDALRVGMGSGSICITÖEVMACGRPQGTAVYKVAEYARRFQVP	360		
Oy	361	VIADGGIQNVGHIKALALGASTVMMGSLAATTEAPGEYFFSDGIRKKYRGMSLDAM	420		
Db	361	IADGGIQTVGHVVKALALGASTVMMGSLAATTEAPGEYFFSDGVRLKKYRGMSLDAM	420		
Oy	421	DKHLSSÖNRYFSEADKIKVAÖGVSGAVODKSGSIHKFVRYLIAIGIÖHSCÖDIGAKSLTÖVR	480		
Db	421	EKSSSSÖKRYFSEGDVKKIAÖGVSGSIÖDKSGSIÖKFVRYLIAIGIÖHSCÖDIGARSLVLR	480		
Oy	481	AMMYSGELKFEKRTSSAÖVEGVHSLHSYEKRLF	514		
Db	481	SMMYSGELKFEKRTMSAÖIEGVHGLHSYEKRLY	514		

RESULT 5
S41064
IMP dehydrogenase (EC 1.1.1.205) imph - fruit fly (Drosophila melanogaster)
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydroge
C:Species: Drosophila melanogaster
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: S41064; S61482
R:Sifiri, C.D.; Wilson, K.; Smolik, S.; Forte, M.; Ullman, B.
Biochim. Biophys. Acta 1217, 103-106, 1994
A:Title: Cloning and sequence analysis of a Drosophila melanogaster cDNA encoding IMP
A:Reference number: S41064; MUID:94114565; PMID:7904480
A:Accession: S41064
A:Molecule type: mRNA
A:Residues: 1-537 <SITE>
A:Cross-references: EMBL:L22608; NID:g348101; PIDN:AAA16839.1; PID:g348102
R:Nash, D.; Hu, S.; Leonard, N.J.; Tjong, S.Y.K.; Phillips, D.
Genome 37, 333-344, 1994
A:Title: The raspberry locus of Drosophila melanogaster includes an inosine monophosp
A:Accession: S61482; MUID:94259281; PMID:7911114

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-537 <NAS>
A:Cross-references: EMBL:U14847; NID:g290245; PIDN:AAA21831.1; PID:g387594
C:Genetics:
A:Gene: *impdh*
A:Cross-references: FlyBase:FBgn0003204
A:Map position: 10
A:Introns: 55/2; 105/3; 323/1; 503/2
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F:52-118/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:139-189/Domain: CBS homology <CBS1>
F:203-251/Domain: CBS homology <CBS2>
F:252-499/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:350/Active site: Cys #status predicted

Query Match	67.48;	Score 1764.5;	DB 1;	Length 537;
Best Local Similarity	68.08;	Pred. No. 1.7e-106;		
Matches 342;	Conservative 72;	Mismatches 82;	Indels 7;	Gaps 3;

[illegible]

RESULT 6
S59508
IMP dehydrogenase (EC 1.1.1.205) ras - fruit fly (*Drosophila* sp.)
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: *Drosophila* sp.
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: S59508
R:Slee, R.; Bownes, M.
Mol. Gen. Genet. 248, 755-766, 1995
A:Title: The raspberry locus encodes *Drosophila* inosine monophosphate dehydrogenase.
A:Reference number: S59508; MUID:96069715; PMID:7476879
A:Accession: S59508

A:Molecule type: mRNA
A:Residues: 1-537 <SLE>
A:Cross-references: GB:S80430; NID:g1245860; PIDN:AAE35628.1; PID:g1245861
C:Genetics:
A:Gene: FLYBase:ras
A:Cross-references: FLYBase:FBgn0003204
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:52-117/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:138-189/Domain: CBS homology <CBS1>
F:202-249/Domain: CBS homology <CBS2>
F:250-499/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:350/Active site: Cys #status predicted

Query Match	62.4%;	Score 1635.5;	DB 1;	Length 537;
Best Local Similarity	64.5%;	Pred. No. 3.7e-98;		
Matches 325;	Conservative 73;	Mismatches 95;	Indels 11;	Gaps 6;

QY	17	GLTAQÖLFENCGDGLTYNDFLILPGYIDFTADQÖVDLTSAITKKITLKTPLVSSPMDTVEA	76
Db	39	GLSCKELFÖNONGEGLPYNDFLILPGYIDFTAEVDDLSSPLTKSLTLRAPLVSSPMDTVTES	98
QY	77	GMAIAMALTGGIGIFIHNCPTPEFANEVRKVKYEOGFITDPVVLSPKDRVRDVEAKAR	136
Db	99	-RCHAMALCGGIGIIHNCPTPEXÖALEVHKVKYKHGFMRDPSVMSPTNTVGDLVLEARRK	157
QY	137	HGFCGPIPTDTGRMGSRVLGVISSRDIDFLKEEHDCELEIMTKREDLVVAPRSITLKE	196
Db	158	NGFTGYPTENGKLGKLLGMVTSRAIDF-RENÖPESSLADIMT--TELVTA PNGINLP	214
QY	197	ANEILÖRSKKGLPIVNEDEDELVAITARTDLKKNRDYPLASKDAKKÖLLCGAICTHEDD	256
Db	215	EHAILEKSRKA-TAIVNÖAGELVAMIA RADLKKARSYPNASKDSNTRLLCPAICTRSED	273
QY	257	K-YRLDLLAÖAGVDVVLDDSSÖGNSIFÖIMIKYIKDKYPNLÖVIGNVVTAÖAKNLI	314
Db	274	KGCRALALLVRNGVDVITLDDSSÖGNSVIOVEMIKYIKETYPBELÖVITGNNVTRAÖAKNLI	333
QY	315	DAGVDALRYGMSGSGSICITÖEVNACGRPÖATAVYKVEYARREFGVPVIADGGIONVGHIA	374
Db	334	DAGVDGLRGMGSGSICITÖEVNACGCPÖATAVYÖVSTYARÖFGVPVIADGGIHAIGHIV	393
QY	375	KALALGASTYVMGSLLAATTEAPEBEFFSDGIRLKKYRGMSLDAMD---KHLSÖNRY	430
Db	394	KATALGASAVYMMGSLLAGTSEAPBEFFSDGVRLKKYRGMSLEAMERGDAKGAMSRYIY	453
QY	431	FSEADKIVYÖGVS GAVÖDKGSINKFVPLYIAGIQHSCÖDIGAKSLTÖVRAMYSGELKF	490
Db	454	HNEMDKMYAÖGVSGSIVDKGSYVRLPYLECGLÖHSCÖDIGANSINKLRDMYNGÖLRF	513
QY	491	EKRTSSAÖVEGGVHSLHSYKRLF	514
Db	514	MKRTHSAÖLEGNVHGLFSYKRLF	537

RESULT 7
S50890
IMP dehydrogenase (EC 1.1.1.205) YML056c - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YW958.06c
C:Species: *Saccharomyces cerevisiae*
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 19-Apr-2002
C:Accession: S50890
R:Devlin, K.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49800
A:Accession: S50890
A:Molecule type: DNA
A:Residues: 1-524 <DEV>
A:Cross-references: EMBL:Z46729; NID:g577134; PIDN:CAAB6719.1; PID:g577140; GSPDB:GN0
C:Genetics:

A:Gene: SGD:IMD4; MIPS:YML056C
A:Cross-references: SGD:S0004520
A:Map position: 13L
A:Introns: 154/1
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:38-104/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:188-236/Domain: CBS homology <CBS>
F:237-485/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:336/Active site: Cys #status predicted

Query Match 61.5%; Score 1610.5; DB 1; Length 524;
Best Local Similarity 61.8%; Pred. No. 1.5e-96;
Matches 316; Conservative 82; Mismatches 102; Indels 11; Gaps 5;

QY 11 SYVPDDGLTAQOLF--CGDGLTYNDLFLPGYIDFTADQVDLTSLTKKITLKTPLVSS 68
Db 17 TYSSKDGLSVQELMDSTTRGGLTYNDFLVPLGLVNFPPSSAVSLQTKLTKKITLNTPEVSS 76
QY 69 PMDTVTEAGMALAMALTGGIGFIHNCTPEFQANEVRKKYKKEOGFTDPVVLSPKDRVR 128
Db 77 PMDTVTEADMAIYMALGGIGFIHNCTPKEQASMKVKMFENGFINSPVISPPTTVG 136
QY 129 DVEFAKARHFGCGIPITDTGRMGSRVGISSRDIDFLKEEHDCELEIMTKREDLVVA 188
Db 137 EVKVMKRKFGFSGPVTEDGKCPKGLVLTSDIQFL--EDDSLVSSEVMTKNP--VTG 192
QY 189 PRSITLKEANEILQRSKKGLPIVNEDEDLVAIARTDLKKNRDYPLASKDA--KKQLLGC 247
Db 193 IKGITLKEGNEILKQTKKGLLIYDNGNLVMSLRADLMKNQNYPLASKSATTKQLLGC 252
QY 248 AAIQTHEDDKYRLDLAQAGVDVVLDSQGSNIFQINMIKYIKDKYFNLOVIGNVVTA 307
Db 253 AAIQTLEADKERLRLVEAGLDVVLDSQGSNVSFQINMIKIKETFPDLEIIAGNVATR 312
QY 308 AQAKNLIDAGVDALRVGMSGISICIQEVLACGRPOATAVYKVEYARREGVPVIADGCI 367
Db 313 EQAANLIAAGADGLRIGMSGISICITQEVMACGRPOGTAVVNYCQFANDEGVPAMDAGV 372
QY 368 QNVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM---DKH 423
Db 373 QNIGHTTKALALGSSVTVMGCMLAGTTESPEGEYFYKDGKRLKAYRGMGSTIDAMQKTGNKG 432
QY 424 LSSQNRYSSEADKIKVAQVSGAVQDKGSIHKFVPLYLIAGIQHSCQDIPEAKSLTOVRAMM 483
Db 433 NASTSRYSSESQSVLVAQVSGAVVDKGSIKKFIPLYLNGLQHSQDIPCESLTSLKENV 492
QY 484 YSGELKFEKRTSSAQVEGCVHSLHSEYKRLF 514
Db 493 QNGEVRFEFRTASAOLEGCVHNLHSEYKRLY 523

RESULT 8
S59402
IMP dehydrogenase (EC 1.1.1.205) YLR432w - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein L9553.4
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 19-Apr-2002
C:Accession: S59402
R:Du, Z.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9753.
A:Reference number: S53391
A:Accession: S59402
A:Molecule type: DNA
A:Residues: 1-523 <DUZ>
A:Cross-references: EMBL:U21094; NID:g665967; PIDN:AAB67516.1; PID:g665971; GSPDB:GN0001
A:Experimental source: strain S288C (AB972)
C:Genetics:
A:Gene: SGD:IMD3; MIPS:YLR432w

A:Cross-references: SGD:S0004424
A:Map position: 12R
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:187-235/Domain: CBS homology <CBS>
F:236-484/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:335/Active site: Cys #status predicted

Query Match 61.4%; Score 1607.5; DB 1; Length 523;
Best Local Similarity 62.2%; Pred. No. 2.3e-96;
Matches 314; Conservative 81; Mismatches 99; Indels 11; Gaps 5;

QY 16 DGLTAQOLF--CGDGLTYNDLFLPGYIDFTADQVDLTSLTKKITLKTPLVSSPMDTV 73
Db 21 DGLSVQELMDSKTRGGLTYNDFLVPLGLVDPESSSEVSLQTKLIRNITLNTPEVSSPMDTV 80
QY 74 TEAGMALAMALTGGIGFIHNCTPEFQANEVRKKYKKEOGFTDPVVLSPKDRVRDVFEA 133
Db 81 TESEMAIFMALLGIGIGFIHNCTPEQADMVRRVKNYENGFINNPVISPPTTVGFAKSM 140
QY 134 KARHFGCGIPITDTGRMGSRVGISSRDIDFLKEEHDCELEIMTKREDLVVAPRSIT 193
Db 141 KERFGFSGPVTEDGKRNGLMGIVTSRDIQFV--EDNSLLVQDVMTKNP--VTGAQGIT 196
QY 194 LKEANEILQRSKKGLPIVNEDEDLVAIARTDLKKNRDYPLASKDA--KKQLLGAATGT 252
Db 197 LSEGNEILKIKKIGKGLLIYDNGNLVMSLRDLMKNQNYPLASKSATTKQLLGAATGT 256
QY 253 HEDDKYRLDLAQAGVDVVLDSQGSNIFQINMIKYIKDKYFNLOVIGNVVTAQAQKN 312
Db 257 IDADKERLRLVEAGLDVVLDSQGSNVSFQINMIKIKETFPDLEIIAGNVATREQAN 316
QY 313 LIDAGVDALRVGMSGISICIQEVLACGRPOATAVYKVEYARREGVPVIADGCIQNVGH 372
Db 317 LIAAGADGLRIGMSGISICITQEVMACGRPOGTAVVNYCEFANGFICPMADGGVQNGH 376
QY 373 IAKALALGASTVMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM---KHLSSQN 428
Db 377 ITKALALGSSVTVMGCMLAGTTESPEGEYFYQDGKRLKAYRGMGSIDAMQKTGTGNASTS 436
QY 429 RYFSEADKIKVAQVSGAVQDKGSIHKFVPLYLIAGIQHSCQDIPEAKSLTOVRAMMSGEL 488
Db 437 RYFSESQSVLVAQVSGAVVDKGSIKKFIPLYLNGLQHSQDIPCESLTSLKENVQSKV 496
QY 489 KFEKRTSSAQVEGCVHSLHSEYKRL 513
Db 497 RFEFRTASAOLEGCVHNLHSEYKRL 521

RESULT 9
S48997
IMP dehydrogenase (EC 1.1.1.205) PUR5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YHR216w
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 19-Apr-2002
C:Accession: S48997
R:Macri, C.
submitted to the EMBL Data Library, February 1994
A:Description: The sequence of S. cerevisiae cosmid 9177.
A:Reference number: S48997
A:Accession: S48997
A:Molecule type: DNA
A:Residues: 1-523 <MAC>
A:Cross-references: EMBL:U00029; NID:g551322; PIDN:AAB69728.1; PID:g458916; GSPDB:GNO
C:Genetics:
A:Gene: SGD:IMD2; PUR5; MIPS:YHR216w
A:Cross-references: SGD:S0001259
A:Map position: 8R
C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule c
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:187-235/Domain: CBS homology <CBS>
F:236-484/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:335/Active site: Cys #status predicted

Query Match 60.7%; Score 1589.5; DB 1; Length 523;
Best Local Similarity 61.2%; Pred. No. 3.3e-95;
Matches 309; Conservative 84; Mismatches 101; Indels 11; Gaps 5;

QY 16 DGLTAQQLFN--CGDGLTYNDFLLPGYIDFTADQVDLTSAITKTKITLKPVLVSSPMDTV 73
Db 21 DGLSVQELMSKIRGGLTYNDFLLPGLVDFASSEVSLQTKLTRNTLTNIPLVSSPMDTV 80
QY 74 TEAGMAIAMALTGGIGIFIHNCPTPEQANEVRKKVKKYEQGFITDPVVLSPKDRVDFEA 133
Db 81 TESEMATFMALGGIGIFIHNCPTPEQADMVRRVKNYENGFINNPVISPPTTVGEAKSM 140
QY 134 KARHFGCGIPITDTGRMGSRVLGIISSRIDFLKEEHDCFLKEIMTKREDLVVAPRSIT 193
Db 141 KEKYGFAGFPVTTDGKRNAAKLVGITSRDIOFV--EDNSLLVQDVMTKNP--VTGAQGIT 196
QY 194 LKEANEILQRSKKGLPIVNEDELVAIARTDLKKNRDYPLASKDAK-KQLLGAAGT 252
Db 197 LSEGNELKRLKKGRLLLVNDEKGNLVSMLSRITLDMKNQNYPLASKSANTKQLLGAAGT 256
QY 253 HEDDKYRLDLLAQAGVDVVLDDSSQNSIFQINMIKIKDKYPNLOVIGNVVTAQAQKN 312
Db 257 MDADKERLRLVAKGLDVVLDDSSQNSIFELMLKWKVESFPGLEVIAAGNVVTRQAAAN 316
QY 313 LIDAGVDALRVGMSGSGSICIIOEVLACGRPOATAVYKYVEYARRFGVPVIADGGIQNVGH 372
Db 317 LIAAGADGLRIGMGTSICITQOEVMACGRPOGTAVYNVCEPANQFVPCMADGGVQNIQH 376
QY 373 IAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMD---KHLSSQN 428
Db 377 ITKALALGSSIVMMGMLAGTTESPEYFYQDGKRLKAYRGMGSIDAMQKTGKGNASTS 436
QY 429 RYFSEADKIKVAQGVSGAVODKGIHKFVPLYLAGIQHSCODIGAKSLTQVRAMYSSEL 488
Db 437 RYFSESDVLAQGVSGAVVDKSGIKRIPLYLNGLQHSQODIGCRSLTLKNNVQRGKV 496
QY 489 KFEKRTSSAOVEGGVHSLHSYEKRL 513
Db 497 RFEFRTASQLEGGVHNLHSYEKRL 521

RESULT 10
T40127
IMP dehydrogenase (EC 1.1.1.205) SPBC2F12.14c - fission yeast (Schizosaccharomyces pombe
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenas
C:Species: Schizosaccharomyces pombe
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C:Accession: T40127; T42083
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z21907
A:Accession: T40127
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-524 <MOO>
A:Cross-references: EMBL:Z97211; PIDN:CAB10161.1; GSPDB:GN00067; SPDB:SPBC2F12.14c
A:Experimental source: strain 972h-; cosmid c2F12
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T42083
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 62-252, 'G', 254-262, 'P', 264-293 <YOS>
A:Cross-references: EMBL:D89106; NID:g1749419; PIDN:BAAL3769.1; PID:g1749420
A:Experimental source: strain PR745
C:Genetics:
A:Gene: SPDB:SPBC2F12.14c
A:Map position: 2
A:introns: 153/1
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:124-174/Domain: CBS homology <CBS1>
F:187-237/Domain: CBS homology <CBS2>
F:238-486/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:337/Active site: Cys #status predicted

Query Match 56.3%; Score 1473.5; DB 1; Length 524;
Best Local Similarity 58.0%; Pred. No. 1.1e-87;
Matches 296; Conservative 77; Mismatches 128; Indels 9; Gaps 4;

QY 12 YVPDDGLTAQQLF--NCGDGLTYNDFLLPGYIDFTADQVDLTSAITKTKITLKPVLVSSP 69
Db 17 YEKKDGLSIDDLIRHNFQGLTFENDFLIPGYIDFVPNNVSLERISRNIVLKTPEWSSP 76
QY 70 MDVTTEAGMAIAMALTGGIGIFIHNCPTPEQANEVRKKVKKYEQGFITDPVVLSPKDRVRD 129
Db 77 MDVTTEQMAIYMALLGIGIVIHNCPTPEQAAAMVRKKVKKYENGFIIDPVVFSQHTVGD 136
QY 130 VFEAKARHFGCGIPITDTGRMGSRVLGIISSRIDFLKEEHDCFLKEIMTKREDLVVAP 189
Db 137 VLKIKETKGFSGIPITENGKLRGKLIVGIVTSRDVQFHKDTNP--VTEVMTPRELITVA 194
QY 190 RSITLKEANEILQRSKKGLPIVNEDELVAIARTDLKKNRDYPLASKDA-KKQLLGA 248
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QY 309 QAKNLIDAGVDALRVGMSGSGSICIIOEVLACGRPOATAVYKYVEYARRFGVPVIADGGIQ 368
Db 315 QTASLIAAGADGLRVGMSGSACITQEVMACGRPOATAIAQVAEFASQFGIGVIADGGIQ 374
QY 369 NVGHIAKALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMD---KHL 424
Db 375 NVGHMVKSLSGATAVMMGGLLAGTTESPEYFYVREGQRYKSYRGMGSIAAMEGTGVNKN 434
QY 425 SSQNRIFYSEADKIKVAQGVSGAVQDKGIHKFVPLYLAGIQHSCODIGAKSLTQVRAMMY 484
Db 435 ASTGRYFSENDAVRVAQGVSGLVVDKGSLLRFLPLYLTGLQHALQDIDGKTSLDELHEAVD 494
QY 485 SGELKFEKRTSSAOVEGGVHSLHSYEKRL 514
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RESULT 11
A55407
IMP dehydrogenase (EC 1.1.1.205) - Trypanosoma brucei brucei
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH)
C:Species: Trypanosoma brucei brucei
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 16-Jul-1999
C:Accession: A55407
R:Wilson, K.; Berens, R.L.; Sifri, C.D.; Ullman, B.
J. Biol. Chem. 269, 28979-28987, 1994
A:Title: Amplification of the inosinate dehydrogenase gene in Trypanosoma brucei gamb
A:Reference number: A55407; MUID:95050714; PMID:7961861
A:Accession: A55407
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 20:31:00 ; Search time 1209 Seconds
(without alignments)
11436.455 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 2000000000

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41: em_htgo_other:*

Pred. No. is the number of results predicted by change to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1450	87.7	1654	9 HUMIMP	J04208 Human inosi
2	1438	86.9	1642	6 ARI41889	ARI41889 Sequence
3	1438	86.9	1642	6 I06570	I06570 Sequence 1
4	1178	71.2	1663	9 BC006124	BC006124 Homo sapi
5	1172	70.9	1648	9 BC012840	BC012840 Homo sapi
6	1170	70.7	1655	9 BC015567	BC015567 Homo sapi
7	615	37.2	1158	6 AX418035	AX418035 Sequence
8	613	37.1	1158	6 AX418036	AX418036 Sequence
9	612	37.0	1155	6 AX418030	AX418030 Sequence
10	612	37.0	1155	6 AX418031	AX418031 Sequence
11	612	37.0	1155	6 AX418032	AX418032 Sequence
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13	612	37.0	1158	6 AX418037	AX418037 Sequence
14	396	23.9	396	6 AX093346	AX093346 Sequence
15	242	14.6	6193	6 AX409550	AX409550 Sequence
16	242	14.6	6193	9 HUMIMPDH	L33842 Homo sapien
17	209	12.6	10557	9 HUMIMP	L39210 Homo sapien
18	137	8.3	1851	9 BC009321	BC009321 Homo sapi
19	88	5.3	360	9 HUMIMPDEH	L08114 Human inosi
20	62	3.7	1614	10 CRUIMP	J04209 Chinese ham
21	62	3.7	1620	6 ARI41890	ARI41890 Sequence
22	62	3.7	1620	6 I06572	I06572 Sequence 3
23	56	3.4	1545	10 MUSIMPDA	M98333 Mus musculu
24	56	3.4	1680	10 BC010314	BC010314 Mus muscu
25	56	3.4	1707	10 MUSIMPD	M33934 Mouse IMP d
26	56	3.4	182658	2 AC084743	AC084743 Mus muscu
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28	53	3.2	332	9 HS86C2R	Z66268 H.sapiens C
29	51	3.1	51	6 AX190186	AX190186 Sequence
30	41	2.5	393	6 ARI41893	ARI41893 Sequence
31	41	2.5	393	6 ARI41894	ARI41894 Sequence
32	41	2.5	393	6 I06574	I06574 Sequence 5
33	39	2.4	114558	2 AC107280	AC107280 Rattus no
34	39	2.4	160331	2 AC129612	AC129612 Rattus no
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36	33	2.0	168808	2 AC103220	AC103220 Rattus no
37	30	1.8	44	6 ARI19642	ARI19642 Sequence
38	29	1.8	687	9 HUMYO19A04	AF075074 Homo sapi
39	28	1.7	6193	6 AX348472	AX348472 Sequence
40	28	1.7	114558	2 AC107280	AC107280 Rattus no
41	26	1.6	42	6 ARI19643	ARI19643 Sequence
42	26	1.6	50	6 AX190187	AX190187 Sequence
43	26	1.6	51	6 AX190185	AX190185 Sequence
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45	25	1.5	51	6 AX190184	AX190184 Sequence
46	24	1.5	33	6 AX418042	AX418042 Sequence
47	23	1.4	30	6 AX418045	AX418045 Sequence
48	23	1.4	344	6 ARI41891	ARI41891 Sequence
49	23	1.4	344	6 ARI41892	ARI41892 Sequence
50	23	1.4	344	6 I06573	I06573 Sequence 4

ALIGNMENTS

RESULT 1	
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LOCUS	
DEFINITION	HUMIMP 1654 bp mRNA linear PRI 11-JUN-1993
ACCESSION	J04208
VERSION	J04208.1 GI:186391
KEYWORDS	inosine-5'-monophosphate dehydrogenase.
SOURCE	Human peripheral blood leukocyte, cDNA to mRNA, clone HIMP.
ORGANISM	Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 1654)
TITLE Collart,F.R. and Huberman,E.
JOURNAL Cloning and sequence analysis of the human and Chinese hamster
MEDLINE J. Biol. Chem. 263 (30), 15769-15772 (1988)
PUBMED 89008491
COMMENT Draft entry and computer-readable sequence for [1] kindly provided by F.R.Collart, 22-AUG-1988.
FEATURES Location/Qualifiers
source 1..1654
/organism="Homo sapiens"
/db_xref="taxon:9606"
48..1592
/note="inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)"
/codon_start=1
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/db_xref="GI:307066"
/translation="MADYLISGTSYVPDGLTAAQLFNGDGLTVNDFLLPGYIDF
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RDIDFLKEEHDCFLLEIMTKREDLVVAPRSITLKEANEILQRSKGRKLPVNEDEL
VAIARTDLKNRDYPPLASKDAKKQLCGAIGTHEDDKYRLDLAQAGYDVVVLDS
QGNISFQIMIKYIKDKYPNLQVIGNVVTAQAKNLIDAGVDALRYGMSGICITQ
EVLACGRPQATAVYKVSSEYARFVPIADGIIQNVGHIAKALALGASIVYMMGSLAA
TTEAPGEYFSDGIRLKRKRGMSLDAMDRLSSQNRIFYSEADKIKVAQGVSGAVODK
GSIHKFVPIYIAGIQHSCQDIGAKSLTQVRAMMYSGLKFEKRTSSADYEGVHSLHS
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BASE COUNT 415 a 418 c 451 g 370 t
ORIGIN 45 bp upstream of Ball site.

Query Match 87.7%; Score 1450; DB 9; length 1654;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1650; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 241 TGGTTTCTCTCCATGACACAGTCACAGAGGCTGGGATGGCCATAGCAATGGCGCTTA 300

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QY 841 AGCGTGTGTGATGTAGTGGTTTGGACTCTTCCAGGCAAAATCCATCTTCCAGATCA 900
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QY 1141 GAGGAATCCAAAAATGTGGGTCAATATTGCGAAAGCCTTGGCCCTTGGGCTCCACAGTCA 1200
Db 1141 GAGGAATCCAAAAATGTGGGTCAATATTGCGAAAGCCTTGGCCCTTGGGCTCCACAGTCA 1200

QY 1201 TGATGGCTCTCTCTCGGTGCCACCACCTGAGGCCCTGGTGAATACTCTTTTCCGATG 1260
Db 1201 TGATGGCTCTCTCTCGGTGCCACCACCTGAGGCCCTGGTGAATACTCTTTTCCGATG 1260

QY 1261 GGATCCGGCTAAAGAAATATCGGGGTATGGGTTCTCTGATGCCATGACAAGCAGCTCA 1320
Db 1261 GGATCCGGCTAAAGAAATATCGGGGTATGGGTTCTCTGATGCCATGACAAGCAGCTCA 1320

QY 1321 GCAGCGAAGACAGATATTTCAGTGAAGCTGACAAATCAAAAGTGGCCAGGAGTGTCTG 1380
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Db 1621 TTTTTCATATAAAGTTTAGAAGACCCGAATTTC 1654

RESULT 2
AR141889
LOCUS AR141889 1642 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6147194.
ACCESSION AR141889
VERSION AR141889.1 GI:15101405
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1642)
AUTHORS Collart,F.R. and Huberman,E.
TITLE Eukaryotic IMPDH polynucleotide and antibody compositions
JOURNAL Patent: US 6147194-A 1 14-NOV-2000;
FEATURES
source 1. 1642
location/Qualifiers
BASE COUNT 411 a 416 c 449 g 366 t
ORIGIN

Query Match 86.9%; Score 1438; DB 6; length 1642;
Best Local Similarity 99.8%; Pred.No. 0;
Matches 1638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GGGCGTCTCTGGAGACACGCGGGGTGTCCTGTGTGGCCATGGCCG ACTACCTGATTA 66
Db 1 GGGCGTCTCTGGAGACACGCGGGGTGTCCTGTGTGGCCATGGCCG ACTACCTGATTA 60
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Db 1621 CAATAAAAGTTTAGAAGACCC 1642

RESULT 3
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DEFINITION Sequence 1 from Patent WO 9001545.

ACCESSION 106570
VERSION 106570.1 GI:589653
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1642)
AUTHORS Collart,F.R. and Huberman,E.
TITLE METHOD AND MATERIALS RELATING TO IMPDH AND GMP PRODUCTION
JOURNAL Patent: WO 9001545-A 1 22-FEB-1990;
FEATURES
source 1..1642
location/Qualifiers
BASE COUNT 411 a 416 c 449 g 366 t
ORIGIN
Query Match 86.9%; Score 1438; DB 6; Length 1642;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GGGGGTCTCGGAGACACGCGGTGTCCTGTGTGGCCATGCCGACTACCTGATTA 66
Db 1 GGGGGTCTCGGAGACACGCGGTGTCCTGTGTGGCCATGCCGACTACCTGATTA 60
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Db 781 GGGCAGGCAATTGGCACTCATGAGGATGACAAGTATAGGCTGCACTTGCTCGCCAGGCTG 840
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RESULT 4
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LOCUS BC006124
DEFINITION Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone
ACCESSION MGCL13021 IMAGE:3545693, mRNA, complete cds.
VERSION BC006124
KEYWORDS BC006124.1 GI:13543972
SOURCE MGC.
ORGANISM Homo sapiens.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1663)

AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yardi Butlerfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutscher, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stolt, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 18 Row: f Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.

FEATURES
source location/Qualifiers

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YEKRLF"

BASE COUNT 436 a 412 c 448 g 367 t
ORIGIN

Query Match 71.2%; Score 1178; DB 9; Length 1663;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 69 GGGGCGACGTCCTACGTGCGCAGACGCGACTCACAGCAGCAGCTC TCACTGCGGA 128
Db 62 GGGGCGACGTCCTACGTGCGCAGACGCGACTCACAGCAGCAGCTC TCACTGCGGA 121

QY 129 GACGCTCACCTACATGACTTTCTCATTCCTGGGTACATCGAC TCACTGCGAG 188
Db 122 GACGCTCACCTACATGACTTTCTCATTCCTGGGTACATCGAC TCACTGCGAG 181

QY 189 CAGGTGACCTGACTTCTGCTGTGACCAAGAAAATCACTCTTAAGACCCCACTGGTTGCC 248
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QY 969 GCGCCAGGCCAAGAACCTCATTTGATGAGGCTGTGATGCCCTGCGGGGTGGGCATGGGAAGT 1028
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QY	1329	AACAGATATTTCAGTGAAGCTGCACAAATCAAAGTGGCCAGGGAGTGTCTGTGTGTG	1388
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QY	1389	CAGGACAAAGGTCATCCACAAATTTGTCCCTTACCTGATTTGCTGGCATCCAACACTCA	1448
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QY	1509	CTTAAGTTGAGAAGAGAACGTCCTCAGCCCAGGTGGAAGGTGGCGTCCATAGCCTCCAT	1568
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Db	1622	ATAAAGTTTAGAAGA	1638

RESULT 5	
BC012840	
LOCUS	BC012840
DEFINITION	Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone MGC:9332 IMAGE:3447994, mRNA, complete cds.
	1648 bp mRNA linear PRI 22-AUG-2001

ACCESSION	BC012840
VERSION	BC012840.1
KEYWORDS	GI:15277479
SOURCE	MG.
ORGANISM	Homo sapiens.
	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1648)
Strausberg, R.
Direct Submission
Submitted (20-AUG-2001) National Institutes of Health, Mammalian

REMARK	COMMENT
Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAK Plate: 12 Row: a Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

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Best Local Similarity	99.48;	Pred. No. 0;		
Matches 1622; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

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QY	135	CTCACCTACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACAGGTG	194
Db	121	CTCACCTACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACAGGTG	180
QY	195	GACCTGACTTCTGCTCTGACCAGAATAATCACTTTTAAGACCCCACTGGTTTCCCTCTCC	254
Db	181	GACCTGACTTCTGCTCTGACCAGAATAATCACTTTAAGACCCCACTGGTTTCCCTCTCC	240
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QY	435	GTTTTTGAGGGCCAAAGCCCCGGCATGTTTCTGCGGTATCCCAATCACAGACACAGGCCGG	494
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QY	555	GAACATGACTGTTTCTTGGAAAGAGATATGACAAAGAAGGGAAGACTTGGTGTAGCCCC	614
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QY	615	CGCAGCATCACACTGAAGGAGGCAATGAATTCGCAGCGCAGCAAGAAGGAAAAGTTG	674
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Db	1561	GAGAAGCGGCTTTTCTGAAAAGGATCCAGCACACCTCTCGGTTTTTTTCAATAAAA	1620
QY	1635	GTTTAGAAGAAGA 1645	
Db	1621	GTTTAGAAGAAGA 1631	

RESULT 6
BC015567 1655 bp mRNA linear PRI 09-OCT-2001
LOCUS BC015567
DEFINITION Homo sapiens, IMP (inosine monophosphate) dehydrogenase 2, clone MGC:20947 IMAGE:4576285, mRNA, complete cds.

ACCESSION		BC015567
VERSION		BC015567.1 GI:15990411
KEYWORDS		MGC.
SOURCE		Homo sapiens.
ORGANISM		Homo sapiens.
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1 (bases 1 to 1655)
TITLE		Strausberg, R.
JOURNAL		Direct Submission
REMARK		Submitted (04-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
COMMENT		NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: Louis Staudt CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
FEATURES		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 30 Row: j Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
source		Location/Qualifiers 1..1655 /organism="Homo sapiens" /db_xref="LocustID:3615" /db_xref="taxon:9606" /clone="MGC:20947 IMAGE:4576285" /tissue_type="Primary B-Cells from Tonsils" /clone_lib="NIH_MGC_48" /lab_host="DH10B-R" /note="Vector: pOTB7" 41..1585 /codon_start=1 /product="IMP (inosine monophosphate) dehydrogenase 2" /protein_id="AAH15567.1" /db_xref="GI:15990412" /translation="MADYLISGTSYPPDDGLTAQQLFNCGGDGLTYNDFLLPGYIDF TADVDLTSLTKRITLKTPLVSSPMDVTEAGMAIAMALTGIGFIHNNCTPEFOAN EVRKVKYEQGFITDPVLSPKDRVRYFEAKARHFGCGIPITDGRMGSRVLGIISS RDIDFLKEEHDFLEIMTKREDLVVAPAGITLKEANEILORSKRGKLPVNEDEL VAIARTDLKKNRDYPLASKDAKKQLCGAIGTHEDDKYRLDLAAGVDVVLDSS OGNSIFOINMILKIKDKYPNLOVIGNVYTAQAOKNLIDAGVDALRYMGSGSICITQ EVLACGRPQATAVYKVEYARFEGVPYIADGIQNVGHIAKALAICASTVMGSLAA TTEAPGEYFSPSDGIRLKKYRGMGSLDAMDKLSSONRYFSEADKIKVAQGVSGAVQDK GSIHKFVPLYLIAGIQHSCQDIDGAKSLTQVRAMVYSGELKFEKRTISSAQVEGVHLSHS YEKRLF"
BASE COUNT		430 a 410 c 450 g 365 t
ORIGIN		
Query Match		70.7%; Score 1170; DB 9; Length 1655;
Best Local Similarity		99.4%; Pred. No. 0;
Matches 1620; Conservative		0; Mismatches 9; Indels 0; Gaps 0;
QY	17	CGGAGACACGCGGGGTGTCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGGCAC 76

Db 10 CGGAGACACGGCGGGTGTCCTGTGTTGGCCATGGCCGACTACCTGATTTAGTGGGGGAC 69
QY 77 GTCTACGTGGCAGACGACGGACTCACAGACAGCAGCTCTTCAACTGCGGAGACGGCCT 136
Db 70 GTCTACGTGGCAGACGACGGACTCACAGACAGCAGCTCTTCAACTGCGGAGACGGCCT 129
QY 137 CACCTACAAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACCAGGTGA 196
Db 130 CACCTACAAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACCAGGTGA 189
QY 197 CCTGACTTCTGCTCTGACCAAGAAAAATCACTCTTAAAGACCCCACTGGTTTCTCTCCAT 256
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Db 310 CATCCACCACAACTGTACACCTGAATTCAGGCCCAATGAAGTTCGGAAGTGAAGAAATA 369
QY 377 TGAACAGGATTCATCACAGACCTGTGTCCTCAGCCCCAAGGATCGCGTGCGGATGT 436
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QY 437 TTTTGAGGCCAAGGCCCGGCATGTTTCTGCGGTATCCCAATCACAGACACAGCCGAT 496
Db 430 TTTTGAGGCCAAGGCCCGGCATGTTTCTGCGGTATCCCAATCACAGACACAGCCGAT 489
QY 497 GGGAGCCGCTTGTGGGCATCATCTCTCCAGGACATTTGATTTTCTCAAGAGAGGA 556
Db 490 GGGAGCCGCTTGTGGGCATCATCTCTCCAGGACATTTGATTTTCTCAAGAGAGGA 549
QY 557 ACATGACTGTTTCTTGAAGAGATAATGACAAGAGGAGACTTGTGTAGCCCCCG 616
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QY 617 CAGCATCACACTGAAGGAGCAATGAATTTCTGCAGCGCAGCAAGAAAGGAAAGTTGCC 676
Db 610 AGGCATCACACTGAAGGAGCAATGAATTTCTGCAGCGCAGCAAGAAAGGAAAGTTGCC 669
QY 677 CATTTGAATGAAAGATGATGAGCTTGTGGCATCATTTGCCCGACAGACCTGAAGAAGAA 736
Db 670 CATTTGAATGAAAGATGATGAGCTTGTGGCATCATTTGCCCGACAGACCTGAAGAAGAA 729
QY 737 TCGGACTACCCACTAGCCTCCAAGATGCCAAGAACAGCTGTGTGTGGGCGAGCCAT 796
Db 730 TCGGACTACCCACTAGCCTCCAAGATGCCAAGAACAGCTGTGTGTGGGCGAGCCAT 789
QY 797 TGGCACTCAATGAGGATGACAAGTATAGGCTGGACTTGCTCGCCCAAGCTGGTGTGATGT 856
Db 790 TGGCACTCAATGAGGATGACAAGTATAGGCTGGACTTGCTCGCCCAAGCTGGTGTGATGT 849
QY 857 AGTGTTTTGGACTCTTCCAGGAGAAATTCATCTTCCAGATCAATATGATCAAGTACAT 916
Db 850 AGTGTTTTGGACTCTTCCAGGAGAAATTCATCTTCCAGATCAATATGATCAAGTACAT 909
QY 917 CAAGACAAATATCCCTAATCTCCAAGTCAATTGGAGGCAATGTGTCTACTGCTGCCAGGC 976
Db 910 CAAGACAAATATCCCTAATCTCCAAGTCAATTGGAGGCAATGTGTCTACTGCTGCCAGGC 969
QY 977 CAAGAACCTCAATTGATGACAGGTGTGATGCCCTGCGGGTGGGCATGGGAAGTGGCTCCAT 1036
Db 970 CAAGAACCTCAATTGATGACAGGTGTGATGCCCTGCGGGTGGGCATGGGAAGTGGCTCCAT 1029
QY 1037 CTGCATTATCCAGGAAGTGTGCTGTGGCGGGCCCAAGCAACAGCAGTGTACAAGGT 1096
Db 1030 CTGCATTATCCAGGAAGTGTGCTGTGGCGGGCCCAAGCAACAGCAGTGTACAAGGT 1089
QY 1097 GTATGATATGACAGGCGCTTGTGTCCGGTCAATTGCTGATGAGAGAAATCCAAATGT 1156
Db 1090 GTACAGATATGACAGGCGCTTGTGTCCGGTCAATTGCTGATGAGAGAAATCCAAATGT 1149

QY 1157 GGGTCATATTGCGAAAGCCTTGGCCCTTGGGGCCTCCACAGTCAATGATGGGCTCTCTCT 1216
Db 1150 GGGTCATATTGCGAAAGCCTTGGCCCTTGGGGCCTCCACAGTCAATGATGGGCTCTCTCT 1209
QY 1217 GGCTGCCACCACTGAGGCCCCCTGGTGAATACTTCTTTTCCGATGGGATCCGGCTAAAGAA 1276
Db 1210 GGCTGCCACCACTGAGGCCCCCTGGTGAATACTTCTTTTCCGATGGGATCCGGCTAAAGAA 1269
QY 1277 ATATCGCGGTATGGGTCTCTCTCGATGCCATGGACAAGCACCTTCAGCCAGACAGATA 1336
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QY 1637 TTAGAAAGA 1645
Db 1630 TTAGAAAGA 1638
RESULT 7
AX418035 1158 bp DNA linear PAT 18-JUN-2002
LOCUS AX418035 Sequence 45 from Patent WO0185952.
DEFINITION AX418035
ACCESSION AX418035
VERSION AX418035.1 GI:21523082
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Krystek,S.R., Sheriff,S., Wiltner,M.R., Hollenbaugh,D.L., Yan,N.,
Mouravieff,J.E., Einspahr,H.M. and Kish,R.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and
uses thereof
JOURNAL Patent: WO 0185952-A 45 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source 1..1158
BASE COUNT 279 a 301 c 310 g 268 t
ORIGIN
Query Match 37.2%; Score 615; DB 6; Length 1158;
Best local Similarity 99.5%; Pred. No. 0;
Matches 815; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 774 CAGCTGCTGTGTGGGCGAGCCATTTGCCACTCATGAGGATGACAGATATAGGCTGACTTG 833
Db 340 CAGCTGCTGTGTGGGCGAGCCATTTGCCACTCATGAGGATGACAGATATAGGCTGACTTG 399
QY 834 CTGCGCCAGCGCTGTGTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCATCTTC 893
Db 1157 GGGTCATATTGCGAAAGCCTTGGCCCTTGGGGCCTCCACAGTCAATGATGGGCTCTCTCT 1216
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QY 1577 GAAGCGGCTTTTCTGAAAAGGGATCCAGCACACCTCCTCGGTTTTTTTTCATATAAAGT 1636
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QY 1637 TTAGAAAGA 1645
Db 1630 TTAGAAAGA 1638
RESULT 7
AX418035 1158 bp DNA linear PAT 18-JUN-2002
LOCUS AX418035 Sequence 45 from Patent WO0185952.
DEFINITION AX418035
ACCESSION AX418035
VERSION AX418035.1 GI:21523082
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Krystek,S.R., Sheriff,S., Wiltner,M.R., Hollenbaugh,D.L., Yan,N.,
Mouravieff,J.E., Einspahr,H.M. and Kish,R.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and
uses thereof
JOURNAL Patent: WO 0185952-A 45 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source 1..1158
BASE COUNT 279 a 301 c 310 g 268 t
ORIGIN
Query Match 37.2%; Score 615; DB 6; Length 1158;
Best local Similarity 99.5%; Pred. No. 0;
Matches 815; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db	400	CTCCCCCAGGCTGGTGTGATGTAGTGCTTTTGGACTCTTCCACAGGGA	AATTCATCTTC	459
QY	894	CAGATCAATATGATCAAGTACATCAAGACAAATACCTTAATCTCCAA	ATCATTTGAGGC	953
Db	460	CAGATCAATATGATCAAGTACATCAAGACAAATACCTTAATCTCCAA	ATCATTTGAGGC	519
QY	954	AATGTGTCACCTGCTGCCACAGGCCAAGAACCTCATTTGATGAGGTGTG	ATGCCCTGGCG	1013
Db	520	AATGTGTCACCTGCTGCCACAGGCCAAGAACCTCATTTGATGAGGTGTG	ATGCCCTGGCG	579
QY	1014	GTGGGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTCTGGCC	GTGGGGGGGCC	1073
Db	580	GTGGGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTCTGGCC	GTGGGGGGGCC	639
QY	1074	CAAGCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCCTTTGGT	ATTCCGGTCATT	1133
Db	640	CAAGCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCCTTTGGT	ATTCCGGTCATT	699
QY	1134	GCTGATGGAGGAATCCAAAATGGGTCATATTGCGAAAGCCTTGGCC	TTGGGGGCTCC	1193
Db	700	GCTGATGGAGGAATCCAAAATGGGTCATATTGCGAAAGCCTTGGCC	TTGGGGGCTCC	759
QY	1194	ACAGTCATGATGGGCTCTCTCTGGCTGCCACACCTGAGGCCCTGGT	TAATACTTCTTT	1253
Db	760	ACAGTCATGATGGGCTCTCTCTGGCTGCCACACCTGAGGCCCTGGT	TAATACTTCTTT	819
QY	1254	TCCGATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCGAT	ATCATGACAAG	1313
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QY	1314	CACCTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAAATCAAA	ATGGCCACAGGA	1373
Db	880	CACCTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAAATCAAA	ATGGCCACAGGA	939
QY	1374	GTGCTGTGCTGTGTGACAGACAAAGGGTCAATCCACAATTTGTCCCT	ACCTGATTGCT	1433
Db	940	GTGCTGTGCTGTGTGACAGACAAAGGGTCAATCCACAATTTGTCCCT	ACCTGATTGCT	999
QY	1434	GGCATCCAACTCATGCGCAGACATTTGGTCCCAAGAGCTTGACCCAA	ATCCGAGCCATG	1493
Db	1000	GGCATCCAACTCATGCGCAGACATTTGGTCCCAAGAGCTTGACCCAA	ATCCGAGCCATG	1059
QY	1494	ATGTAATCTCTGGGAGCTTAAGTTTGAGAAGAGAAGCGTCTCAGCCCA	ATGGAAGGTGGC	1553
Db	1060	ATGTAATCTCTGGGAGCTTAAGTTTGAGAAGAGAAGCGTCTCAGCCCA	ATGGAAGGTGGC	1119
QY	1554	GTCCATAGCCTCCATTCGTATGAGAAGCGGCTTTTCTGA	1592	
Db	1120	GTCCATAGCCTCCATTCGTATGAGAAGCGGCTTTTCTGA	1158	

RESULT 8
AX418036 1158 bp DNA linear PAT 18-JUN-2002
LOCUS AX418036
DEFINITION Sequence 46 from Patent WO0185952.
ACCESSION AX418036
VERSION AX418036.1 GI:21523083
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Krystek,S.R., Sheriff,S., Witmer,M.R., Hollenbush,D.L., Yan,N., Mouravieff,J.E., Einspahr,H.M. and Kish,K.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and uses thereof
JOURNAL Patent: WO 0185952-A 46 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source 1..1158
/organism="Homo sapiens"
/db_xref="taxon:9606"

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Query Match	37.1%; Score 613; DB 6; Length 1158;								
Best Local Similarity	99.5%; Pred. No. 0;								
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Db	342	GCTGCTGTGTGGGGCAGCCATTGGCACTCATGAGGATGACAAGTATAGGCTGGACTTGC	401						
QY	836	CGCCCAAGCTGTGTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCATCTTCCA	895						
Db	402	CGCCCAAGCTGTGTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCATCTTCCA	461						
QY	896	GATCAATATGATCAAGTACATCAAGACAACAATACCTTAATCTCCAAGTCAATGGAGCAA	955						
Db	462	GATCAATATGATCAAGTACATCAAGACAACAATACCTTAATCTCCAAGTCAATGGAGCAA	521						
QY	956	TGTGCTCACTGCTGCCAGGCCAAGACCTCATTTGATGACAGGTGTGATGCCCTGGCGGT	1015						
Db	522	TGTGCTCACTGCTGCCAGGCCAAGACCTCATTTGATGACAGGTGTGATGCCCTGGCGGT	581						
QY	1016	GGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGCTGGCCCTGGGGCCCCA	1075						
Db	582	GGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGCTGGCCCTGGGGCCCCA	641						
QY	1076	AGCAACAGCAGTGTACAAAGGTGTATGAGTATGCACGGCGCTTTGGTTCGGGTCAATTGC	1135						
Db	642	AGCAACAGCAGTGTACAAAGGTGTATGAGTATGCACGGCGCTTTGGTTCGGGTCAATTGC	701						
QY	1136	TGATGGAGGAATCCAAAATGTGGGTCAATTGCGAAAGCCTTGGCCCTTGGGGCTTCCAC	1195						
Db	702	TGATGGAGGAATCCAAAATGTGGGTCAATTGCGAAAGCCTTGGCCCTTGGGGCTTCCAC	761						
QY	1196	AGTCATGATGGGCTCTCTCTGGCTGCCACCACTGAGGCCCTTGGTGAATACTTCTTTTC	1255						
Db	762	AGTCATGATGGGCTCTCTCTGGCTGCCACCACTGAGGCCCTTGGTGAATACTTCTTTTC	821						
QY	1256	CGATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGACAAGCA	1315						
Db	822	CGATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGACAAGCA	881						
QY	1316	CCTCAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAAATCAAAAGTGGCCAGGAGT	1375						
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QY	1376	GTCTGTGCTGTGACAGACAAGGTCATCCACAAATTTGTCCCTTACCTGATTGCTGG	1435						
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QY	1436	CATCCAACACTCATGCCAGGACATTGGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGAT	1495						
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QY	1556	CCATAGCCTCCATTCGTATGAGAAGCGGCTTTTCTGA	1592						
Db	1122	CCATAGCCTCCATTCGTATGAGAAGCGGCTTTTCTGA	1158						

RESULT 9
AX418030 1155 bp DNA linear PAT 18-JUN-2002
LOCUS AX418030
DEFINITION Sequence 40 from Patent WO0185952.
ACCESSION AX418030
VERSION AX418030.1 GI:21523077
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.									
AUTHORS	1 Krystek,S.R., Sheriff,S., Wilmer,M.R., Hollenbaugh,D.L., Yan,N., Mouravieff,J.E., Einspahr,H.M. and Kish,K.									
TITLE	Modified inosine 5'-monophosphate dehydrogenase polypeptides and uses thereof									
JOURNAL	Patent: WO 0185952-A 40 15-NOV-2001;									
FEATURES	Bristol-Myers Squibb Co. (US)									
source	Location/Qualifiers									
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BASE COUNT	/organism="Homo sapiens"									
ORIGIN	/db_xref="taxon:9606"									
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Query Match	37.0%; Score 612; DB 6; Length 1155;									
Best Local Similarity	99.5%; Pred. No. 0;									
Matches	812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
QY	777	CTGCTGTGTGGGGCAGCCATTGGC	ACTCATGAGGATGACAACTATAGGCTGGACTTGCTC	836						
Db	340	CTGCTGTGTGGGGCAGCCATTGGC	ACTCATGAGGATGACAACTATAGGCTGGACTTGCTC	399						
QY	837	GCCCCAGGCTGGTGTGGATGTAGTGGTTTGGACTCTTCCAGGGAATTCATCTTCCAG	896							
Db	400	GCCCCAGGCTGGTGTGGATGTAGTGGTTTGGACTCTTCCAGGGAATTCATCTTCCAG	459							
QY	897	ATCAATATGATCAAGTACATCAAGACAATAACCTAATCTCCAAAGTCATTGGAGGCAAT	956							
Db	460	ATCAATATGATCAAGTACATCAAGACAATAACCTAATCTCCAAAGTCATTGGAGGCAAT	519							
QY	957	GTGGTCACTGCTGCCAGGCCAAGAACCCTCATTTGATGTCAGGTGTGATGCCCTGCGGGTG	1016							
Db	520	GTGGTCACTGCTGCCAGGCCAAGAACCCTCATTTGATGTCAGGTGTGATGCCCTGCGGGTG	579							
QY	1017	GGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCCCTGTGGCGGCCCAA	1076							
Db	580	GGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCCCTGTGGCGGCCCAA	639							
QY	1077	GCAACAGCAGTGTACAAGGTGTATGAGTATGCACGGCGCTTGTGTTCCGGTCAATTGCT	1136							
Db	640	GCAACAGCAGTGTACAAGGTGTCAAGATATGCACGGCGCTTGTGTTCCGGTCAATTGCT	699							
QY	1137	GATGAGGAATCCAAATGTGGGTCAATATTTGCGAAAGCCTTGCCCTTGGGGCTCCACA	1196							
Db	700	GATGAGGAATCCAAATGTGGGTCAATATTTGCGAAAGCCTTGCCCTTGGGGCTCCACA	759							
QY	1197	GTCATGATGGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCTGTGTAATACTTCTTTCC	1256							
Db	760	GTCATGATGGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCTGTGTAATACTTCTTTCC	819							
QY	1257	GATGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCCTCGATGCCATGGACAAGCAC	1316							
Db	820	GATGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCCTCGATGCCATGGACAAGCAC	879							
QY	1317	CTCAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATTCAAAGTGGCCAGGGAGTG	1376							
Db	880	CTCAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATTCAAAGTGGCCAGGGAGTG	939							
QY	1377	TCTGTGCTGTGACAGCAAAAGGCTCAATCCACAATTTGTCCCTTACCTGATTTGCTGGC	1436							
Db	940	TCTGTGCTGTGACAGCAAAAGGCTCAATCCACAATTTGTCCCTTACCTGATTTGCTGGC	999							
QY	1437	ATCCAACACTCATGCCAGGACATTTGGTGC	1496							
Db	1000	ATCCAACACTCATGCCAGGACATTTGGTGC	1059							
QY	1497	TACTCTGGGAGCTTAAGTTTGAGAAGAGAACGCTCTCTACGCCCAAGGTGGAAGGTGGCGTC	1556							
Db	1060	TACTCTGGGAGCTTAAGTTTGAGAAGAGAACGCTCTCTACGCCCAAGGTGGAAGGTGGCGTC	1119							
QY	1557	CATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA	1592							

Db	1120	CATAGCCTCCATTCGTATGAGAAGCGCTTTCTG	1155	
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AX418031				
LOCUS	AX418031	1155 bp	DNA	linear
DEFINITION	Sequence 41 from Patent WO0185952.			
ACCESSION	AX418031			
VERSION	AX418031.1	GI:21523078		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	1			
AUTHORS	Krystek,S.R., Sherif,S., Wiltner,M.R., Hollenbaugh,D.L., Yan,N., Mouravieff,J.E., Einspahr,H.M. and Kish,K.			
TITLE	Modified inosine 5'-monophosphate dehydrogenase polypeptides and uses thereof			
JOURNAL	Patent: WO 0185952-A 41 15-NOV-2001;			
FEATURES	Bristol-Myers Squibb CO. (US)			
source	Location/Qualifiers			
	1. 1155			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
BASE COUNT	278 a 300 c 310 g 267 t			
ORIGIN				
Query Match	37.0%;	Score 612;	DB 6;	Length 1155;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 812;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	777	CTGCTGTGCGGCAGCCATTTGGCAGTATGAGATGACAAGTATAGGCTGGACTTGCCTC	836	
Db	340	CTGCTGTGTGGGCAGCCATTGGCAGTATGAGATGACAAGTATAGGCTGGACTTGCCTC	399	
QY	837	GCCCAGGCTGTGTGATGTAGTGGTTTGGACTCTTCCAGGGAATTTCCATCTTCCAG	896	
Db	400	GCCCAGGCTGTGTGATGTAGTGGTTTGGACTCTTCCAGGGAATTTCCATCTTCCAG	459	
QY	897	ATCAATATGATCAAGTACATCAAAAGACAATACCCCTAATCTTCCAGTATGGAGGCAAT	956	
Db	460	ATCAATATGATCAAGTACATCAAAAGACAATACCCCTAATCTTCCAGTATGGAGGCAAT	519	
QY	957	GTGTCACCTGCTGCCAGGCCAAGACCTCATTTGATGACAGTGTGATGCCCTGCGGCTG	1016	
Db	520	GTGTCACCTGCTGCCAGGCCAAGACCTCATTTGATGACAGTGTGATGCCCTGCGGCTG	579	
QY	1017	GGCATGGGAAGTGCGCTCCATCTGCATTATCCAGGAAGTGCTGCGCTGCGGCGCCCAA	1076	
Db	580	GGCATGGGAAGTGCGCTCCATCTGCATTATCCAGGAAGTGCTGCGCTGCGGCGCCCAA	639	
QY	1077	GCAACAGCAGTGTACAAGGTGTATGAGTATGCACGCGCTTTGGTGTCCGGTCAATTGCT	1136	
Db	640	GCAACAGCAGTGTACAAGGTGTCAAGTATGCACGCGCTTTGGTGTCCGGTCAATTGCT	699	
QY	1137	GATGAGGAATCCAAATATGTGGGTCAATTTGCGAAGAGCCCTTGGGCCCTTCCACA	1196	
Db	700	GATGAGGAATCCAAATATGTGGGTCAATTTGCGAAGAGCCCTTGGGCCCTTCCACA	759	
QY	1197	GTCATGATGGGCTCTCTCCTGGCTGCGCACCACTGAGGCGCCCTGCTGAATACTTCTTTCC	1256	
Db	760	GTCATGATGGGCTCTCTCCTGGCTGCGCACCACTGAGGCGCCCTGCTGAATACTTCTTTCC	819	
QY	1257	GATGGATCGCGCTTAAGAATAATCGCGGTATGGGTTCTCTCGATGCCATGACAAGCAC	1316	
Db	820	GATGGATCGCGCTTAAGAATAATCGCGGTATGGGTTCTCTCGATGCCATGACAAGCAC	879	
QY	1317	CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATCAAGTGGGCCAGGAGTG	1376	
Db	880	CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATCAAGTGGGCCAGGAGTG	939	

QY 1377 TCTGTCGTCGTGCAGGACAAAGGCTCAATCCACAATTGTCCCTTACCTGATTGCTGGC 1436
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Db 940 TCTGGTGTCTGTGCAGGACAAAGGCTCAATCCACAATTGTCCCTTACCTGATTGCTGGC 999
QY 1437 ATCCAACACTCATGCCAGGACATTTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATG 1496
|||||
Db 1000 ATCCAACACTCATGCCAGGACATTTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATG 1059
QY 1497 TACTCTGGGGAGCTTAAAGTTTGAGAAGAACGCTCTCAGCCCCAGGTGSAAGGTGGCGTC 1556
|||||
Db 1060 TACTCTGGGGAGCTTAAAGTTTGAGAAGAACGCTCTCAGCCCCAGGTGSAAGGTGGCGTC 1119
QY 1557 CATAGCCTCCATTTCGTATGAGAAGCGGCTTTTCTGA 1592
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Db 1120 CATAGCCTCCATTTCGTATGAGAAGCGGCTTTTCTGA 1155

RESULT 11
AX418032 1155 bp DNA linear PAT 18-JUN-2002
LOCUS AX418032
DEFINITION Sequence 42 from Patent WO0185952.
ACCESSION AX418032
VERSION AX418032.1 GI:21523079
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Krystek,S.R., Sheriff,S., Wiltner,M.R., Hollenbaugh,D.L., Yan,N.,
Mouravieff,J.E., Einspahr,H.M. and Kish,K.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and
uses thereof
JOURNAL Patent: WO 0185952-A 42 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source 1. .1155
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 277 a 299 c 312 g 267 t
ORIGIN

Query Match 37.0%; Score 612; DB 6; Length 1155;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 777 CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGCTTGACTTGCTC 836
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Db 340 CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGCTTGACTTGCTC 399
QY 837 GCCCAGGCTGTGTGATGTAGTGTGTTTGACTCTTCCAGGGAATCCATCTTCCAG 896
|||||
Db 400 GCCCAGGCTGTGTGATGTAGTGTGTTTGACTCTTCCAGGGAATCCATCTTCCAG 459
QY 897 ATCAATATGATCAAGTACATCAAGAACAATACCCTAATCTCCAAGTC TTGAGGCAAT 956
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Db 460 ATCAATATGATCAAGTACATCAAGAACAATACCCTAATCTCCAAGTC TTGAGGCAAT 519
QY 957 GTGTCACCTGCTGCCAGGCCAAGAACTCATTTGATGACAGGTGGATCCCTGCGGTG 1016
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Db 520 GTGTCACCTGCTGCCAGGCCAAGAACTCATTTGATGACAGGTGGATCCCTGCGGTG 579
QY 1017 GGCATGGAGAGTGGCTCCATCTGCATTAATCCAGGAAGTGTGGCTGTGGCGGCCCAA 1076
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Db 580 GGCATGGAGAGTGGCTCCATCTGCATTAATCCAGGAAGTGTGGCTGTGGCGGCCCAA 639
QY 1077 GCAACAGCACTGTACAAGGTGTATGATGACAGGCGCTTTGGCTTCGCTCATTTGCT 1136
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Db 640 GCAACAGCACTGTACAAGGTGTATGATGACAGGCGCTTTGGCTTCGCTCATTTGCT 699
QY 1137 GATGAGGAATCCAAATGTGGGTATTTGCGAAAGCCTTGCGCCCTTGCGGCTCCACA 1196
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Db 700 GATGAGGAATCCAAATGTGGGTATTTGCGAAAGCCTTGCGCCCTTGCGGCTCCACA 759

QY 1197 GTCATGATGGGCTCTCTCTCGCTGGCCACCACTGAGGCCCTGGTGAATACTTCTTTCC 1256
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Db 760 GTCATGATGGGCTCTCTCTCGCTGGCCACCACTGAGGCCCTGGTGAATACTTCTTTCC 819
QY 1257 GATGGATCCCGCTAAAGAATATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCAC 1316
|||||
Db 820 GATGGATCCCGCTAAAGAATATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCAC 879
QY 1317 CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATATCAAGTGGCCAGGAGTG 1376
|||||
Db 880 CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATATCAAGTGGCCAGGAGTG 939
QY 1377 TCTGTCGTCGTGCAGGACAAAGGCTCAATCCACAATTTGTCCCTTACCTGATTGCTGGC 1436
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Db 940 TCTGTCGTCGTGCAGGACAAAGGCTCAATCCACAATTTGTCCCTTACCTGATTGCTGGC 999
QY 1437 ATCCAACACTCATGCCAGGACATTTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATG 1496
|||||
Db 1000 ATCCAACACTCATGCCAGGACATTTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATG 1059
QY 1497 TACTCTGGGGAGCTTAAAGTTTGAGAAGAACGCTCTCAGCCCCAGGTGGAAGGTGGCGTC 1556
|||||
Db 1060 TACTCTGGGGAGCTTAAAGTTTGAGAAGAACGCTCTCAGCCCCAGGTGGAAGGTGGCGTC 1119
QY 1557 CATAGCCTCCATTTCGTATGAGAAGCGGCTTTTCTGA 1592
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Db 1120 CATAGCCTCCATTTCGTATGAGAAGCGGCTTTTCTGA 1155

RESULT 12
AX418033 1155 bp DNA linear PAT 19-JUN-2002
LOCUS AX418033
DEFINITION Sequence 43 from Patent WO0185952.
ACCESSION AX418033
VERSION AX418033.1 GI:21523080
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Krystek,S.R., Sheriff,S., Wiltner,M.R., Hollenbaugh,D.L., Yan,N.,
Mouravieff,J.E., Einspahr,H.M. and Kish,K.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and
uses thereof
JOURNAL Patent: WO 0185952-A 43 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source 1. .1155
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 278 a 300 c 309 g 268 t
ORIGIN

Query Match 37.0%; Score 612; DB 6; Length 1155;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 777 CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGCTC 836
|||||
Db 340 CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGCTC 399
QY 837 GCCCAGGCTGTGTGATGTAGTGTGTTTGACTCTTCCAGGGAATTCATCTTCAG 896
|||||
Db 400 GCCCAGGCTGTGTGATGTAGTGTGTTTGACTCTTCCAGGGAATTCATCTTCAG 459
QY 897 ATCAATATGATCAAGTACATCAAGAACAATACCCTAATCTCCAAGTATGGAGGCAAT 956
|||||
Db 460 ATCAATATGATCAAGTACATCAAGAACAATACCCTAATCTCCAAGTATGGAGGCAAT 519
QY 957 GTGTCACCTGCTGCCAGGCCAAGAACTCATTTGATGACAGGTGTGATGCGGCTGGGTG 1016
|||||

Db	520	GTGGTCACTGCTGCCCCAGGCCACAAGACCTCATGTGATGCAGGTGTGGATGGCCCTGCGGGTG	579
QY	1017	GGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGTGGCTGTGGCGGCCCCAA	1076
Db	580	GGCATGGGAAGTGGCTCCATCTGCATTTACCGCAGGAAGTGTGGCTGTGGCGGCCCCAA	639
QY	1077	GCAACAGCAGTGTACAAGGTGTATGATATGCACGGCGCTTTGGTGTTCGGGTCAITGCT	1136
Db	640	GCAACAGCAGTGTACAAGGTGTACAGATATGCACGGCGCTTTGGTGTTCGGGTCAITGCT	699
QY	1137	GATGCAGGAATCCAAAATGTGGGTCAITATGCGAAAAGCCTTGGCCCTTGGGGCCTCCACA	1196
Db	700	GATGCAGGAATCCAAAATGTGGGTCAITATGCGAAAAGCCTTGGCCCTTGGGGCCTCCACA	759
QY	1197	GTCATGATGGGCTCTCTCCTGGCTGCCACCACTGAGGCCCTGTGTAATACTTCTTTCC	1256
Db	760	GTCATGATGGGCTCTCTCCTGGCTGCCACCACTGAGGCCCTGTGTAATACTTCTTTCC	819
QY	1257	GATGGGATCCGGCTTAAGAATAATCCGGGTATGGGTCTCTCGATGCCATGACAGCAC	1316
Db	820	GATGGGATCCGGCTTAAGAATAATCCGGGTATGGGTCTCTCGATGCCATGACAGCAC	879
QY	1317	CTCAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATCAAAATCAAAAGTGGCCAGGAGTG	1376
Db	880	CTCAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATCAAAATCAAAAGTGGCCAGGAGTG	939
QY	1377	TCTGGTGTCTGTGCAGGACCAAAAGGTCAATCCACAAATTTGTCCCTTACCTGATGTGCTGGC	1436
Db	940	TCTGGTGTCTGTGCAGGACCAAAAGGTCAATCCACAAATTTGTCCCTTACCTGATGTGCTGGC	999
QY	1437	ATCCAACACTCATGCCAGGACATTTGGTGCCAAGACTTGACCCCAAGTCCGAGCCATGATG	1496
Db	1000	ATCCAACACTCATGCCAGGACATTTGGTGCCAAGACTTGACCCCAAGTCCGAGCCATGATG	1059
QY	1497	TACTCTGGGAGCTTAAAGTTTGAGAAGAGAACGTCCTCAGCCCAAGTGAAGGTGGCGTC	1556
Db	1060	TACTCTGGGAGCTTAAAGTTTGAGAAGAGAACGTCCTCAGCCCAAGTGAAGGTGGCGTC	1119
QY	1557	CATAGCCTTCATTCGTATGAGAAGCGGCTTTTCTGA	1592
Db	1120	CATAGCCTTCATTCGTATGAGAAGCGGCTTTTCTGA	1155

RESULT 13
AX418037
LOCUS AX418037 1158 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 47 from Patent WO0185952.
ACCESSION AX418037
VERSION AX418037.1 GI:21523084
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Krystek, S.R., Sheriff, S., Witmer, M.R., Hollenbaugh, D.L., Yan, N.,
Mouravieff, J.E., Einspahr, H.M. and Kish, K.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and
uses thereof
JOURNAL Patent: WO 0185952-A 47 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source 1.1158
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 279 a 301 c 309 g 269 t
ORIGIN

Query Match 37.0%; Score 612; DB 6; Length 1158;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 777 CTGCTGTGTGGGCGAGCCATTGGCATTGAGGATGACAAGTATAGCTGGACTTGCTC 836

Db	343	CTGCTGTGTGGGGCAGCCATTTGGCACATGAGGATGACAAGTATAGGCTGGACTTGGCTC	402
QY	837	GCCCCAGGCTGTGTGGATGTAGTGGTTTGGACTCTTCCAGGGAATTCATCTTCCAG	896
Db	403	GCCCCAGGCTGTGTGGATGTAGTGGTTTGGACTCTTCCAGGGAATTCATCTTCCAG	462
QY	897	ATCAATATGATCAAGTACATCAAAAGACAATACCCTAATCTCCAAGTCATTTGAGGCAAT	956
Db	463	ATCAATATGATCAAGTACATCAAAAGACAATACCCTAATCTCCAAGTCATTTGAGGCAAT	522
QY	957	GTGTCTACTGCTGCCAGGCCAAGAACCTCATTTGATGACAGGTGTGATGCCCTGGGGTG	1016
Db	523	GTGTCTACTGCTGCCAGGCCAAGAACCTCATTTGATGACAGGTGTGATGCCCTGGGGTG	582
QY	1017	GGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGTGCTGGCCTGTGGGGGCCCAA	1076
Db	583	GGCATGGGAAGTGGCTCCATCTGCATTTACGCAGGAAGTGTGCTGGCCTGTGGGGGCCCAA	642
QY	1077	GCAACAGCAGTGTACAAAGGTGTATGAGTATGCACGGCGCTTTGGTGTTCGGTCAATTGCT	1136
Db	643	GCAACAGCAGTGTACAAAGGTGTACAGTATGCACGGCGCTTTGGTGTTCGGTCAATTGCT	702
QY	1137	GATGGAGGAATCCAAAAATGTGGGTCAATATTGGGAAAGCCTTGGCCCTTGGGGCCTCCACA	1196
Db	703	GATGGAGGAATCCAAAAATGTGGGTCAATATTGGGAAAGCCTTGGCCCTTGGGGCCTCCACA	762
QY	1197	GTCATGATGGGCTCTCTCTGGCTGCCACCACTGAAGCCCCCTGGTGAATACTTCTTTTCC	1256
Db	763	GTCATGATGGGCTCTCTCTGGCTGCCACCACTGAAGCCCCCTGGTGAATACTTCTTTTCC	822
QY	1257	GATGGATCCGGCTAAAGAAATATCGCGGTATGCGGTCTCTCGATGCCATGACAAGCAC	1316
Db	823	GATGGATCCGGCTAAAGAAATATCGCGGTATGCGGTCTCTCGATGCCATGACAAGCAC	882
QY	1317	CTCAGCAGCCAGACAAGATATTTCAAGTGAAGCTGACAAATAATCAAAAGTGGCCAGGAGTG	1376
Db	883	CTCAGCAGCCAGACAAGATATTTCAAGTGAAGCTGACAAATAATCAAAAGTGGCCAGGAGTG	942
QY	1377	TCTGGTGCTGTGCAGGACAAGGGTCAATCCACAATTTGTGCCCTTACCTGATTTGCTGGC	1436
Db	943	TCTGGTGCTGTGCAGGACAAGGGTCAATCCACAATTTGTGCCCTTACCTGATTTGCTGGC	1002
QY	1437	ATCCAACACTCATGCCCAGGACATTTGGTGCACAAGCCTTGACCCCAAGTCCGAGCCATGATG	1496
Db	1003	ATCCAACACTCATGCCCAGGACATTTGGTGCACAAGCCTTGACCCCAAGTCCGAGCCATGATG	1062
QY	1497	TACTCTGGGAGCTTAACTTTGAGAAGAGAAGCCTTCAAGCCAGAGTGGAAGGTGGCGTC	1556
Db	1063	TACTCTGGGAGCTTAACTTTGAGAAGAGAAGCCTTCAAGCCAGAGTGGAAGGTGGCGTC	1122
QY	1557	CATAGCCTCCATTGCTATGAGAAGCGGCTTTTCTGA	1592
Db	1123	CATAGCCTCCATTGCTATGAGAAGCGGCTTTTCTGA	1158

RESULT 14
AX093346
LOCUS AX093346 396 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 164 from Patent WO0118046.
ACCESSION AX093346
VERSION AX093346.1 GI:13509795
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 396)
AUTHORS Xu, J. and Stolk, J.A.
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A 164 15-MAR-2001;
CORIXA CORPORATION (US)

FEATURES
location/Qualifiers

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source          1. .396
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
BASE COUNT      96 a      119 c      96 g      85 t
ORIGIN
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Query Match      23.9%; Score 396; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 7e-223;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 21 GACACGCGGCGGTGCTCTGTGTTGGCCATGGCCGACTACCTGATTAGTGGGGCAGCTCC 80
DB 1 GACACGCGGCGGTGCTCTGTGTTGGCCATGGCCGACTACCTGATTAGTGGGGCAGCTCC 60

QY 81 TAGGTGCCAGACGACGGACTCACAGACAGCAGCTCTTCAACTGGGAGACGGCCCTCACC 140
DB 61 TAGGTGCCAGACGACGGACTCACAGACAGCAGCTCTTCAACTGGGAGACGGCCCTCACC 120

QY 141 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACAGGTTGACCTG 200
DB 121 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACAGGTTGACCTG 180

QY 201 ACTTCTGCTCTGACCAAGAAATACATCTTAAGACCCCACTGGTTCCCTCCCATGGAC 260
DB 181 ACTTCTGCTCTGACCAAGAAATACATCTTAAGACCCCACTGGTTCCCTCCCATGGAC 240

QY 261 ACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGCTTACAGGCGCTATTGGCTTCATC 320
DB 241 ACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGCTTACAGGCGCTATTGGCTTCATC 300

QY 321 CACCACAACCTGTACACCTGAATTCAGGCCAATGAAGTTCGGAAGTGAAGAATATGAA 380
DB 301 CACCACAACCTGTACACCTGAATTCAGGCCAATGAAGTTCGGAAGTGAAGAATATGAA 360

QY 381 CAGGATTCATCACAGACCCCTGTGGTCTCAGCCCC 416
DB 361 CAGGATTCATCACAGACCCCTGTGGTCTCAGCCCC 396
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RESULT 15
AX409550      6193 bp      DNA      linear      PAT 14-JUN-2002
DEFINITION    Sequence 2197 from Patent WO0229103.
ACCESSION     AX409550
VERSION       AX409550.1 GI:21442255
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1
AUTHORS      Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE        Gene expression profiles in liver cancer
JOURNAL      Patent: WO 0229103-A 2197 11-APR-2002;
               GENE LOGIC INC (US)
FEATURES
source        1. .6193
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /note="EMBL/GenBank Accession No. L33842"
BASE COUNT    1404 a      1597 c      1628 g      1564 t
ORIGIN
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Query Match      14.6%; Score 242; DB 6; Length 6193;
Best Local Similarity 100.0%; Pred. No. 2.2e-131;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1101 GAGTATGACGCGGCTTTGGTGTTCGCTCATTTGCTGATGAGCAATC AAAATGTGGGT 1160
DB 5210 GAGTATGACGCGGCTTTGGTGTTCGCTCATTTGCTGATGAGCAATC AAAATGTGGGT 5269

QY 1161 CATATTGCGAAGCCTTGGCCCTTGGGCGCTCCACAGTCATGATGGCC CTCTCCTGGCT 1220
DB 5269 CATATTGCGAAGCCTTGGCCCTTGGGCGCTCCACAGTCATGATGGCC CTCTCCTGGCT 1220
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DB 5270 CATATTGCGAACCCTTGGCCCTTGGGCGCTCCACAGTCATGATGGGCTCTCTCTGGCT 5329
QY 1221 GCCACCACCTGAGGCCCCCTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATAT 1280
DB 5330 GCCACCACCTGAGGCCCCCTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATAT 5389

QY 1281 CGCGGTATGGCTTCTCTCGATGCGCATGACAGCACCCTCAGCAGCAGCAGCAAGATATTTC 1340
DB 5390 CGCGGTATGGCTTCTCTCGATGCGCATGACAGCACCCTCAGCAGCAGCAGCAAGATATTTC 5449

QY 1341 AG 1342
DB 5450 AG 5451
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RESULT 16
HUMIMPDH
LOCUS          HUMIMPDH      6193 bp      DNA      linear      PRI 22-MAY-1995
DEFINITION    Homo sapiens (clone FFE-7) type II inosine monophosphate
               dehydrogenase (IMPDH2) gene, exons 1-13, complete cds.
ACCESSION     L33842
VERSION       L33842.1 GI:602457
KEYWORDS      NAD-dependent; differentiation; inosine monophosphate
               dehydrogenase; inosine-5'-monophosphate dehydrogenase; nucleotide
               biosynthesis; proliferation associated gene.
SOURCE        Homo sapiens (tissue library: lambda GEM-11 (Promega)) blood DNA.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 6193)
AUTHORS      Glesne,D.A. and Huberman,E.
TITLE        Cloning and sequence of the human type II IMP dehydrogenase gene
JOURNAL      Biochem. Biophys. Res. Commun. 205 (1), 537-544 (1994)
MEDLINE      95091778
PUBMED       7999076
COMMENT       Related sequences J04208 and L08114.
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               /db_xref="taxon:9606"
               /map="karyotype band P21.2-P24.2"
               /tissue_type="blood"
               /tissue_lib="lambda GEM-11 (Promega)"
               879. .1000
               /gene="IMPDH2"
               /note="minimal promoter"
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               2516. .2722,3385. .3472,3546. .3746,3825. .3914,4014. .4109,
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               /gene="IMPDH2"
               join(983. .1182,1628. .1676,1900. .2001,2110. .2184,
               2516. .2722,3385. .3472,3546. .3746,3825. .3914,4014. .4109,
               5163. .5451,5545. .5688,5769. .5852,5943. .>6005)
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               2516. .2722,3385. .3472,3546. .3746,3825. .3914,4014. .4109,
               5163. .5451,5545. .5688,5769. .5852,5943. .5964)
               /gene="IMPDH2"
               /EC_number="1.1.1.205"
               /codon_start=1
               /product="inosine monophosphate dehydrogenase type II"
               /protein_id="AAA67054.1"
               /db_xref="GI:602458"
               /translation="MADYLISGTSYVPPDGLTAQQLFNCGDGLTYNDPLILPGYIDF
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source        Location/Qualifiers
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               /db_xref="taxon:9606"
               /map="karyotype band P21.2-P24.2"
               /tissue_type="blood"
               /tissue_lib="lambda GEM-11 (Promega)"
               879. .1000
               /gene="IMPDH2"
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               join(983. .1182,1628. .1676,1900. .2001,2110. .2184,
               2516. .2722,3385. .3472,3546. .3746,3825. .3914,4014. .4109,
               5163. .5451,5545. .5688,5769. .5852,5943. .>6005)
               /gene="IMPDH2"
               join(983. .1182,1628. .1676,1900. .2001,2110. .2184,
               2516. .2722,3385. .3472,3546. .3746,3825. .3914,4014. .4109,
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               /gene="IMPDH2"
               983. .1182
               /gene="IMPDH2"
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Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1101 GAGTATGCACGGCGCTTGTGTTCCGGTCATTGCTGATGGAGGAATCCAAATGTGGGT 1160
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Db 5210 GAGTATGCACGGCGCTTGTGTTCCGGTCATTGCTGATGGAGGAATCCAAATGTGGGT 5269
QY 1161 CATATTGCCAAGCCTTGCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCGTGGCT 1220
|||||
Db 5270 CATATTGCCAAGCCTTGCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCGTGGCT 5329
QY 1221 GCCACCACTGAGGGCCCTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATAT 1280
|||||
Db 5330 GCCACCACTGAGGGCCCTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATAT 5389
QY 1281 CGCGGTATGGGTCTCTCGATGCCATGGACAAGCACCCTCAGCAGCCAGAACAGATATTTC 1340
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Db 5390 CGCGGTATGGGTCTCTCGATGCCATGGACAAGCACCCTCAGCAGCCAGAACAGATATTTC 5449
QY 1341 AG 1342
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Db 5450 AG 5451
RESULT 17
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LOCUS
DEFINITION Homo sapiens inosine monophosphate dehydrogenase type II gene,
complete cds.
ACCESSION L39210.1 GI:1702963
VERSION
KEYWORDS inosine monophosphate dehydrogenase; inosine monophosphate
dehydrogenase type II.
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Zimmermann,A.G., Wright,K.L., Ting,J.P. and Mitchell,B.S.
TITLE 1 (bases 1 to 10557)
JOURNAL Characterization of the human inosine-5'-monophosphate
dehydrogenase type II gene
JOURNAL J. Biol. Chem. 270 (12), 6808-6814 (1995)
MEDLINE 95204479
PUBMED 7896827
REFERENCE
AUTHORS Zimmermann,A.G.
TITLE 2 (bases 1 to 10557)
JOURNAL Direct Submission
Submitted (15-NOV-1996) Department of Pharmacology, University of
North Carolina, School of Medicine, CB7365, FLOB, Chapel Hill, NC
27599, USA
REFERENCE
AUTHORS 3 (bases 1 to 10557)
TITLE Zimmermann,A.G., Wright,K.L., Ting,J.P. and Mitchell,B.S.
JOURNAL Regulation of inosine-5'-monophosphate dehydrogenase type II gene
expression in human T cells. Role for a novel 5' palindromic
octamer sequence
J. Biol. Chem. 272 (36), 22913-22923 (1997)
MEDLINE 97426442
PUBMED 9278455
COMMENT On Dec 3, 1996 this sequence version replaced gi:777736.

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	/db_xref="GI:1702964"					
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Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	370	AGAAATATGACAGCGGATTCATCACAGACCCCTGTGCTCCTCAGCCCA	GGATCGCGTGC 429			
Db	3398	AGAAATATGACAGCGGATTCATCACAGACCCCTGTGCTCCTCAGCCCA	GGATCGCGTGC 3457			
QY	430	GGGATGTTTTGAGGCCCAAGCGCCGCATGTTTCTGCGGTATCCCA	CACAGACACAG 489			
Db	3458	GGGATGTTTTGAGGCCCAAGCGCCGCATGTTTCTGCGGTATCCCA	CACAGACACAG 3517			
QY	490	GCCGATGGGAGCGCCCTTGTTGGCATCATCTCTCCAGGACATTG	TTTTCTCAAG 549			
Db	3518	GCCGATGGGAGCGCCCTTGTTGGCATCATCTCTCCAGGACATTG	TTTTCTCAAG 3577			
QY	550	AGGAGGAACATGACTGTTCTTGAAGAG 578				
Db	3578	AGGAGGAACATGACTGTTCTTGAAGAG 3606				
RESULT 18						
LOCUS	BC009321	1851 bp	mRNA linear PRI 12-JUL-2001			
DEFINITION	Homo sapiens, clone MGC:16650 IMAGE:4123521, mRNA, complete cds.					
ACCESSION	BC009321					
VERSION	BC009321.1	GI:14424584				
KEYWORDS	MGC.					
SOURCE	Homo sapiens.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
	Strausberg, R.					
	Direct Submission					
	Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA					
	AUTHORS					
TITLE						
JOURNAL						

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/nisc_mgc/hgri.nih.gov Contact: nisc_mgc@hgri.nih.gov Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Madero, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantirpop, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 26 Row: e Column: 10. Location/Qualifiers 1..1851 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:16650 IMAGE:4123521" /tissue_type="Muscle, rhabdomyosarcoma" /clone_lib="NIH_MGC_17" /lab_host="DH10B-R" /note="Vector: pOTB7" 191..688 /codon_start=1 /product="Unknown (protein for MGC:16650)" /protein_id="AAH09321.1" /db_xref="GI:14424585" /translation="MCYTHALFLQRLPRRSEAGRRPRALRPDVSVARSATVTKSAGLYWRGPDGRLGAVLGDTRRCPLVAMADYLLISGTSYVPPDGLTAQQLFNCGDGLTYKCGPMGLTWAKRGAAPWCKQMGASESRLGRGRGOYSGIGHPPGLTLRHLEKRLGYSEASQ" CDS
BASE COUNT	465 a 551 c 400 g 435 t
ORIGIN	
Query Match	8.3%; Score 137; DB 9; Length 1851;
Best Local Similarity	100.0%; Pred. No. 6.4e-69;
Matches 137; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	9 GCGGTCTCGGAGACACGCGCGGTGCTGTGTTGGCCATGGCCGACTACCTGATTAGT 68
Db	362 GCGGTCTCGGAGACACGCGCGGTGCTGTGTTGGCCATGGCCGACTACCTGATTAGT 421
QY	69 GGGGGCACGTCCTACGTCGCCAGACGAGGACTCACAGCACAGCAGCTCTTCAACTGCCGA 128
Db	422 GGGGGCACGTCCTACGTCGCCAGACGAGGACTCACAGCACAGCAGCTCTTCAACTGCCGA 481
QY	129 GACGGCCTCACCCTACAA 145
Db	482 GACGGCCTCACCCTACAA 498
RESULT 19	
LOCUS	HUMIMPDEH 360 bp DNA linear PRI 12-JUN-1993
DEFINITION	Human inosine 5'-monophosphate dehydrogenase subunit II gene, last 3 exons.
ACCESSION	L08114
VERSION	L08114.1 GI:292239
KEYWORDS	imp dehydrogenase; inosine 5'-monophosphate dehydrogenase dehydrogenase.
SOURCE	Homo sapiens DNA.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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REFERENCE      1 (sites)
AUTHORS        Glesne,D., Collart,F., Varkony,T., Drabkin,H. and Huberman,E.
TITLE          Chromosomal localization and structure of the human type II IMP
                dehydrogenase gene (IMPDH2)
JOURNAL        Genomics 16 (1), 274-277 (1993)
MEDLINE        93252398
PUBMED         8098009
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                exon        140..223
                intron      224..313
                exon        314..360
                3'UTR       333..360
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                ORIGIN
Query Match      5.3%; Score 88; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 9.9e-40;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1486 GAGCCATGATGCTACTCTGGGAGAGCTTAAGTTTGAGAAGAGAAGAGCTTCCTCAGCCCCAGGTGG 1545
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Db   139 GAGCCATGATGCTACTCTGGGAGAGCTTAAGTTTGAGAAGAGAAGAGAGCTTCCTCAGCCCCAGGTGG 198

QY  1546 AAGGTGGCGTCCATAGCCTCCATTGCTA 1573
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Db   199 AAGGTGGCGTCCATAGCCTCCATTGCTA 226

RESULT 20
CRUIIMP        1614 bp      mRNA      linear      ROD 10-JUN-1993
LOCUS          Chinese hamster inosine-5'-monophosphate dehydrogenase (IMP) mRNA,
DEFINITION     complete cds.
ACCESSION      J04209
VERSION        J04209.1 GI:191119
KEYWORDS       inosine-5'-monophosphate dehydrogenase.
SOURCE         Chinese hamster cell line E29Pro+, clone CIMP.
ORGANISM       Cricetulus griseus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                Cricetulus.
REFERENCE      1 (bases 1 to 1614)
AUTHORS        Collart,F.R. and Huberman,E.
TITLE          Cloning and sequence analysis of the human and Chinese hamster
                inosine-5'-monophosphate dehydrogenase cDNAs
JOURNAL        J. Biol. Chem. 263 (30), 15769-15772 (1988)
MEDLINE        89008491
PUBMED         2902093
COMMENT        Draft entry and computer-readable sequence for [1] kindly provided
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Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  306 GGTAATGGCTTCATCCACCACCACTGTACACCTGAATTCCAGGCCAATGAAGTTCGAAA 365
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Db   284 GGTAATGGCTTCATCCACCACCACTGTACACCTGAATTCCAGGCCAATGAAGTTCGAAA 343

QY  366 GT 367
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Db   344 GT 345

RESULT 21
AR141890
LOCUS          AR141890      1620 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION     Sequence 2 from patent US 6147194.
ACCESSION      AR141890
VERSION        AR141890.1 GI:15101406
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 1620)
AUTHORS        Collart,F.R. and Huberman,E.
TITLE          Eukaryotic IMPDH polynucleotide and antibody compositions
JOURNAL        Patent: US 6147194-A 2 14-NOV-2000;
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Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  306 GGTAATGGCTTCATCCACCACCACTGTACACCTGAATTCCAGGCCAATGAAGTTCGAAA 365
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Db   284 GGTAATGGCTTCATCCACCACCACTGTACACCTGAATTCCAGGCCAATGAAGTTCGAAA 343

QY  366 GT 367
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Db   344 GT 345

RESULT 22
LOCUS          106572      1620 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION     Sequence 3 from Patent WO 9001545.
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ACCESSION 106572
VERSION 106572.1 GI:589654
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1620)
AUTHORS Collart,F.R. and Huberman,E.
TITLE METHOD AND MATERIALS RELATING TO IMPDH AND GMP
JOURNAL Patent: WO 9001545-A 3 22-FEB-1990;
FEATURES Location/Qualifiers
source 1..1620
BASE COUNT 423 a 369 c 421 g 407 t
ORIGIN

Query Match 3.7%; Score 62; DB 6; Length 1620;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GGTATGGCTTCATCCACCACTGTACACCTGAATTCCAGCCAAATGAAGTTCCGAAA 365
|||||
DB 284 GGTATGGCTTCATCCACCACTGTACACCTGAATTCCAGCCAAATGAAGTTCCGAAA 343

QY 366 GT 367
||
DB 344 GT 345

RESULT 23
MUSIMPD
LOCUS 1545 bp mRNA linear ROD 27-JUL-1994
DEFINITION Mus musculus IMP dehydrogenase (IMPD) mRNA, complete cds.
ACCESSION M98333
VERSION M98333.1 GI:425157
KEYWORDS IMP dehydrogenase.
SOURCE Mus musculus brain cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1545)
AUTHORS Lightfoot,T. and Snyder,F.F.
TITLE Gene amplification and dual point mutations of mouse IMP dehydrogenase associated with cellular resistance to mycophenolic acid
JOURNAL Biochim. Biophys. Acta 1217 (2), 156-162 (1994)
MEDLINE 94153991
PUBMED 7906545
FEATURES location/Qualifiers
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variation
998

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ORIGIN

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Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 CTGCTGTGTGGGCGCCATTTGGCACTCATGAGGATGACCAAGTATAGGCTGACTT 832
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DB 730 CTGCTGTGTGGGCGCCATTTGGCACTCATGAGGATGACCAAGTATAGGCTGACTT 785

RESULT 24
BC010314 1680 bp mRNA linear ROD 07-AUG-2002
LOCUS

DEFINITION Mus musculus, inosine 5'-phosphate dehydrogenase 2, clone MGC:6193
IMAGE:2646679, mRNA, complete cds.
ACCESSION BC010314
VERSION BC010314.1 GI:16307530
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1680)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amqebcm.tmc.edu
Gunsaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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CDS
998

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EVLACGRPOATAVYKVSEYARRFVPIADGGIQNVGHIAKALALGASTVMMGSLIAA
TTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSONRYFEADKIKVAQVSGAVQDK
GSIHKFVPLYIAGIQHSCQDIGAKSLTQVRAMYSGELKFEKRTSSAQVEGCVHSLHS
YEKRLF"

BASE COUNT 465 a 396 c 435 g 384 t
ORIGIN

Query Match 3.4%; Score 56; DB 10; Length 1680;
Best Local Similarity 100.0%; Pred. No. 9.5e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 CTGCTGTGTGGGCGACCATTTGGCACTCATGAGGATGACACAGTATAGGCTGACTT 832
Db 763 CTGCTGTGTGGGCGACCATTTGGCACTCATGAGGATGACACAGTATAGGCTGACTT 818

RESULT 25
MUSIMPD 1707 bp mRNA linear ROD 12-JUN-1993
LOCUS Mouse IMP dehydrogenase mRNA, complete cds.
DEFINITION M33934
ACCESSION M33934.1 GI:198393
VERSION M33934.1 GI:198393
KEYWORDS IMP dehydrogenase.
SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1707)
AUTHORS Tiedeman,A.A. and Smith,J.M.
TITLE Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase
JOURNAL Gene 97 (2), 289-293 (1991)
MEDLINE 91153661
PUBMED 1671845
COMMENT Draft entry and computer-readable sequence for [Unpublished (1990)]
kindly submitted
by J.M.Smith 27-APR-1990.
Author address:
Dr. J.M. Smith
Seattle Biomedical Research Institute
4 Nickerson St.
Seattle, WA 98109.

FEATURES
source Location/Qualifiers
1..1707
/organism="Mus musculus"
/db_xref="taxon:10090"
67..1611
/note="IMP dehydrogenase (EC 1.2.1.14)"
/codon_start=1
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/translation="MADYLISGTSYVDDGLTAQQLFNCGDGLTYNDFLLPGYIDF
TADQVDLTSA LTKKTLTKPLVSSPMDTVTEAGMAIAMLTGIGIFIHNCTPEFOAN
EVRKVKKYEQGITDPVVLSPKDRVDVFEAKARHGFQGIPIPTDGRMGSRIVGIISS
RDIDFLKEEHDRLFEIMTKREDLVVAPAGVTLKEANEILQRSKKGKLPIVENDEL
VAIIARTDLKKNRDYPLASDAKKQLLGAIGTHEDDKYRLDLLALAGDVVVLDSS
QGNISFQINMIKYEKYPISLOVIGENVTTAAQAKNLIDAGVDALRVGMSGICITQ
EVLACGRPOATAVYKVSEYARRFVPIADGGIQNVGHIAKALALGASTVMMGSLIAA
TTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSONRYFEADKIKVAQVSGAVQDK
GSIHKFVPLYIAGIQHSCQDIGAKSLTQVRAMYSGELKFEKRTSSAQVEGCVHSLHS
YEKRLF"

BASE COUNT 457 a 408 c 451 g 391 t
ORIGIN

Query Match 3.4%; Score 56; DB 10; Length 1707;
Best Local Similarity 100.0%; Pred. No. 9.4e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 CTGCTGTGTGGGCGACCATTTGGCACTCATGAGGATGACACAGTATAGGCTGACTT 832

|||||
Db 796 CTGCTGTGTGGGCGACCATTTGGCACTCATGAGGATGACACAGTATAGGCTGACTT 851

RESULT 26
AC084743/c
LOCUS
DEFINITION AC084743 182658 bp DNA linear HTG 03-FEB-2001
Mus musculus clone RP23-104L6, *** SEQUENCING IN PROGRESS ***
unordered pieces.
AC084743
AC084743.1 GI:11138180
HTG: HTGS_PHASE1.
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 182658)
AUTHORS McCombie,W.R., Baker,J.P., Bahret,A., Bal,H., Balija,V.,
Dedhia,N.N., de la Bastide,M., Huang,E.N., King,L., Kirchoff,K.A.,
Miller,B., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R.,
Rodriguez,S., Santos,L., Shah,R.S., Spiegel,L.A., Toth,K., Vll,M.D.
and Zutavern,T.
TITLE Mouse Genomic Sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 182658)
AUTHORS McCombie,W.R.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-2000) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA

COMMENT
----- Genome Center
Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
Laboratory
Center code: CSHL
Web site: http://www.cshl.org/genseq
Contact: mcombie@cshl.org
----- Project Information
Center project name: RP23-104L6
Center clone name: RP23-104L6

* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1.
9239: contig of 9238 bp in length
9349: gap of unknown length
9350: contig of 7660 bp in length
17010: gap of unknown length
17120: gap of unknown length
17121: contig of 6306 bp in length
23427: gap of unknown length
23537: gap of unknown length
23538: contig of 5952 bp in length
29490: gap of unknown length
29600: gap of unknown length
35374: contig of 5774 bp in length
35485: gap of unknown length
40978: contig of 5493 bp in length
41089: gap of unknown length
46554: contig of 5465 bp in length
46655: gap of unknown length
46666: contig of 5195 bp in length
51861: gap of unknown length
51971: gap of unknown length
57074: contig of 5103 bp in length
57185: gap of unknown length
57186: contig of 4143 bp in length
61329: gap of unknown length
61439: gap of unknown length
61440: contig of 3777 bp in length
65217: gap of unknown length
65328: contig of 3565 bp in length
68893: gap of unknown length
69003: gap of unknown length
69004: contig of 3551 bp in length
72554: contig of 3551 bp in length

*	72555	72665:	gap of unknown length
*	72666	76002:	contig of 3337 bp in length
*	76003	76113:	gap of unknown length
*	76114	79430:	contig of 3317 bp in length
*	79431	79541:	gap of unknown length
*	79542	82808:	contig of 3267 bp in length
*	82809	82919:	gap of unknown length
*	82920	86165:	contig of 3246 bp in length
*	86166	86276:	gap of unknown length
*	86277	89403:	contig of 3127 bp in length
*	89404	89514:	gap of unknown length
*	89515	92609:	contig of 3095 bp in length
*	92610	92720:	gap of unknown length
*	92721	95799:	contig of 3079 bp in length
*	95800	95910:	gap of unknown length
*	95911	98749:	contig of 2839 bp in length
*	98750	98860:	gap of unknown length
*	98861	101564:	contig of 2704 bp in length
*	101565	101675:	gap of unknown length
*	101676	104281:	contig of 2606 bp in length
*	104282	104392:	gap of unknown length
*	104393	106983:	contig of 2591 bp in length
*	106984	107094:	gap of unknown length
*	107095	109664:	contig of 2570 bp in length
*	109665	109775:	gap of unknown length
*	109776	112176:	contig of 2401 bp in length
*	112177	112287:	gap of unknown length
*	112288	114642:	contig of 2355 bp in length
*	114643	114753:	gap of unknown length
*	114754	117092:	contig of 2339 bp in length
*	117093	117203:	gap of unknown length
*	117204	119538:	contig of 2335 bp in length
*	119539	119649:	gap of unknown length
*	119650	121973:	contig of 2324 bp in length
*	121974	122084:	gap of unknown length
*	122085	124406:	contig of 2322 bp in length
*	124407	124517:	gap of unknown length
*	124518	126788:	contig of 2271 bp in length
*	126789	126899:	gap of unknown length
*	126900	129169:	contig of 2270 bp in length
*	129170	129280:	gap of unknown length
*	129281	131544:	contig of 2264 bp in length
*	131545	131655:	gap of unknown length
*	131656	133860:	contig of 2205 bp in length
*	133861	133971:	gap of unknown length
*	133972	136158:	contig of 2187 bp in length
*	136159	136269:	gap of unknown length
*	136270	138445:	contig of 2176 bp in length
*	138446	138556:	gap of unknown length
*	138557	140663:	contig of 2107 bp in length
*	140664	140774:	gap of unknown length
*	140775	142854:	contig of 2080 bp in length
*	142855	142965:	gap of unknown length
*	142966	145037:	contig of 2072 bp in length
*	145038	145148:	gap of unknown length
*	145149	147178:	contig of 2030 bp in length
*	147179	147289:	gap of unknown length
*	147290	149310:	contig of 2021 bp in length
*	149311	149421:	gap of unknown length
*	149422	151406:	contig of 1985 bp in length
*	151407	151517:	gap of unknown length
*	151518	153491:	contig of 1974 bp in length
*	153492	153602:	gap of unknown length
*	153603	155545:	contig of 1943 bp in length
*	155546	155656:	gap of unknown length
*	155657	157584:	contig of 1928 bp in length
*	157585	157694:	gap of unknown length
*	157695	159571:	contig of 1877 bp in length
*	159572	159681:	gap of unknown length
*	159682	161531:	contig of 1850 bp in length
*	161532	161641:	gap of unknown length
*	161642	163442:	contig of 1801 bp in length
*	163443	163552:	gap of unknown length

* 163553 165331: contig of 1779 bp in length
* 165332 165441: gap of unknown length
* 165442 167193: contig of 1752 bp in length
* 167194 167303: gap of unknown length
* 167304 169032: contig of 1729 bp in length
* 169033 169142: gap of unknown length
* 169143 170851: contig of 1709 bp in length
* 170852 170961: gap of unknown length
* 170962 172660: contig of 1699 bp in length
* 172661 172770: gap of unknown length
* 172771 174467: contig of 1697 bp in length
* 174468 174577: gap of unknown length
* 174578 176236: contig of 1659 bp in length
* 176237 176346: gap of unknown length
* 176347 177973: contig of 1627 bp in length
* 177974 178083: gap of unknown length
* 178084 179692: contig of 1609 bp in length
* 179693 179802: gap of unknown length
* 179803 181384: contig of 1582 bp in length
* 181385 181494: gap of unknown length
* 181495 182658: contig of 1164 bp in length.
location/Qualifiers
1.182658
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-104L6"

BASE COUNT 45897 a 42185 c 39609 g 48199 t 6768 others
ORIGIN

Query Match 3.4%; Score 56; DB 2; Length 182658;
Best Local Similarity 100.0%; Pred. No. 6.8e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 777 CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACACAGTATAGGCTGACTT 832
Db 147783 CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACACAGTATAGGCTGACTT 147728

RESULT 27
AC122514 225727 bp DNA linear HTG 30-JUL-2002
LOCUS
DEFINITION Mus musculus chromosome UNK clone RP24-455L10, WORKING DRAFT
AC122514
AC122514.2 GI:22004610
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 225727)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
2 (bases 1 to 225727)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 225727)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (30-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Jul 30, 2002 this sequence version replaced gi:21105978.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0455L10

```
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 224286 bases at least Q40
Consensus quality: 224589 bases at least Q30
Consensus quality: 224737 bases at least Q20
Insert size: 174000; agarose-fp
Quality coverage: 15.05 in Q20 bases; agarose-fp
Quality coverage: 11.65 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 53314: contig of 53314 bp in length
* 53315 53414: gap of unknown length
* 53415 225727: contig of 172313 bp in length.

FEATURES
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    1. 225727
        /organism="Mus musculus"
        /db_xref="taxon:10090"
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        /clone="RP24-455L10"
  misc_feature
    1. 53314
        /note="assembly_name:Contig10"
  misc_feature
    53415. 225727
        /note="assembly_name:Contig11"
  BASE COUNT
    70387 a 42350 c 42349 g 70510 t 131 others
  ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 6.7e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 CTGCTGTGTGGGACGACCATGGACATGAGGATGACACGATATAGGCTTGACTT 832
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Db 110095 CTGCTGTGTGGGACGACCATGGACATGAGGATGACACGATATAGGCTTGACTT 110150

RESULT 28
HS86C2R
LOCUS 332 bp DNA linear PRI 23-OCT-1995
DEFINITION H.sapiens Cpg island DNA genomic Msel fragment, clone 86c2, reverse
            read cpg86c2.r1ta.
ACCESSION Z66268
VERSION Z66268.1 GI:1039090
KEYWORDS Cpg island; genomic Msel fragment.
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 332)
AUTHORS Macdonald,M., Huckle,E., Wilkinson,P. and Micklelem,G.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
REFERENCE 2 (bases 1 to 332)
AUTHORS Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
TITLE Purification of Cpg Islands using a methylated DNA binding column
JOURNAL Nat. Genet. 6 (3), 236-244 (1994)
MEDLINE 94282070
PUBMED 8012384
COMMENT Vector: pGEM-5Zf(-)
        Clones are available from the UK MRC Human Genome Mapping Project
```

```
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.

FEATURES
  source
    1. 332
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="86c2"
        /sex="male"
        /tissue_type="blood"
        /clone_lib="CGI-1"
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  BASE COUNT
    51 a 100 c 119 g 62 t
  ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GACACGGCGGCTGTCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGG 73
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Db 260 GACACGGCGGCTGTCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGG 312

RESULT 29
AX190186/c
LOCUS 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 365 from Patent WO0147942.
ACCESSION AX190186
VERSION AX190186.1 GI:15143562
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL Patent: WO 0147942-A 365 05-JUL-2001;
            Curagen Corporation (US)
FEATURES
  source
    1. 51
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        /db_xref="taxon:9606"
        /note="1 of 2 allelic variants (366 is other
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    12 a 20 c 13 g 6 t
  ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CGGCGGTGTCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGGCAG 77
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Db 51 CGGCGGTGTCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGGCAG 1

RESULT 30
AR141893/c
LOCUS 393 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6147194.
ACCESSION AR141893
VERSION AR141893.1 GI:15101409
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 393)
AUTHORS Collart,F.R. and Huberman,E.
TITLE Eukaryotic IMPDH polynucleotide and antibody compositions
JOURNAL Patent: US 6147194-A 5 14-NOV-2000;
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FEATURES
source 1..393
BASE COUNT 99 a 111 c 89 g 94 t
ORIGIN

Query Match 2.5%; Score 41; DB 6; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.7e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 843 GCTGGTGTGATGTAGTGGTTTGGACTCTTCCACAGGAAA 883
Db 322 GCTGGTGTGATGTAGTGGTTTGGACTCTTCCACAGGAAA 282

RESULT 31
AR141894
LOCUS AR141894 393 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6147194.
ACCESSION AR141894
VERSION AR141894.1 GI:15101410
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 393)
AUTHORS Collart,F.R. and Huberman,E.
TITLE Eukaryotic IMPDH polynucleotide and antibody compositions
JOURNAL Patent: US 6147194-A 6 14-NOV-2000;
FEATURES
source 1..393
/organism="unknown"

BASE COUNT 94 a 89 c 111 g 95 t
ORIGIN

Query Match 2.5%; Score 41; DB 6; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.7e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 843 GCTGGTGTGATGTAGTGGTTTGGACTCTTCCACAGGAAA 883
Db 72 GCTGGTGTGATGTAGTGGTTTGGACTCTTCCACAGGAAA 112

RESULT 32
I06574/c
LOCUS I06574 393 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 9001545.
ACCESSION I06574
VERSION I06574.1 GI:589656
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 393)
AUTHORS Collart,F.R. and Huberman,E.
TITLE METHOD AND MATERIALS RELATING TO IMPDH AND GMP PRODUCTION
JOURNAL Patent: WO 9001545-A 5 22-FEB-1990;
FEATURES
source 1..393
/organism="unknown"

BASE COUNT 99 a 111 c 89 g 94 t
ORIGIN

Query Match 2.5%; Score 41; DB 6; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.7e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 843 GCTGGTGTGATGTAGTGGTTTGGACTCTTCCACAGGAAA 883
Db 322 GCTGGTGTGATGTAGTGGTTTGGACTCTTCCACAGGAAA 282

RESULT 33
AC107280/c
LOCUS AC107280 114558 bp DNA linear HTG 13-JUL-2002
DEFINITION Rattus norvegicus clone CH230-81H4, *** SEQUENCING IN PROGRESS ***,
58 unordered pieces.
AC107280
AC107280.3 GI:21737470
HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 114558)

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkelt,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., Mcleod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogun,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshitari,N., Sisson,I.,
Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tatney,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE

Submitted (18-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 114558)
Worley,K.C.
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE

AUTHORS
TITLE
JOURNAL

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/

Contact:	hgsc-helpebcm.tmc.edu
-----	Project Information
Center project name:	GPEW
Center clone name:	CH230-81H4
-----	Summary Statistics
Sequencing vector:	Plasmid;
Chemistry:	Dye-terminator Big Dye; 100% of reads
Assembly program:	Phrap; version 0.990329
Consensus quality:	59289 bases at least Q40
Consensus quality:	62371 bases at least Q30
Consensus quality:	65704 bases at least Q20

* NOTE:	Estimated insert size may differ from sequence length
* (see	http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE:	This is a 'working draft' sequence. It currently
* consists	of 58 contigs. The true order of the pieces
* is not	known and their order in this sequence record is
* arbitrary.	Gaps between the contigs are represented as
* runs	of N, but the exact sizes of the gaps are unknown.
* This	record will be updated with the finished sequence
* as	soon as it is available and the accession number will
* be	preserved.
* 1	1407: contig of 1407 bp in length
* 1408	1507: gap of unknown length
* 1508	2785: contig of 1278 bp in length
* 2786	2885: gap of unknown length
* 2886	4306: contig of 1421 bp in length
* 4307	4406: gap of unknown length
* 4407	5791: contig of 1385 bp in length
* 5792	5891: gap of unknown length
* 5892	7219: contig of 1328 bp in length
* 7220	7319: gap of unknown length
* 7320	8441: contig of 1122 bp in length
* 8442	8541: gap of unknown length
* 8542	9963: contig of 1422 bp in length
* 9964	10063: gap of unknown length
* 10064	11368: contig of 1305 bp in length
* 11369	11468: gap of unknown length
* 11469	12924: contig of 1456 bp in length
* 12925	13024: gap of unknown length
* 13025	14074: contig of 1050 bp in length
* 14075	14174: gap of unknown length
* 14175	15767: contig of 1593 bp in length
* 15768	15867: gap of unknown length
* 15868	17131: contig of 1264 bp in length
* 17132	17231: gap of unknown length
* 17232	18519: contig of 1288 bp in length
* 18520	18619: gap of unknown length
* 18620	19671: contig of 1052 bp in length
* 19672	19771: gap of unknown length
* 19772	21140: contig of 1369 bp in length
* 21141	21240: gap of unknown length
* 21241	22449: contig of 1209 bp in length
* 22450	22549: gap of unknown length
* 22550	23904: contig of 1355 bp in length
* 23905	24004: gap of unknown length
* 24005	25150: contig of 1146 bp in length
* 25151	25250: gap of unknown length
* 25251	26269: contig of 1019 bp in length
* 26270	26369: gap of unknown length
* 26370	27985: contig of 1616 bp in length
* 27986	28085: gap of unknown length
* 28086	29407: contig of 1322 bp in length
* 29408	29507: gap of unknown length
* 29508	30634: contig of 1127 bp in length
* 30635	30734: gap of unknown length
* 30735	31927: contig of 1193 bp in length
* 31928	32027: gap of unknown length
* 32028	33335: contig of 1308 bp in length
* 33336	33435: gap of unknown length
* 33436	35511: contig of 2076 bp in length
* 35512	35611: gap of unknown length
* 35612	37208: contig of 1597 bp in length

*	37209	37308:	gap of unknown length
*	37309	38952:	contig of 1644 bp in length
*	38953	39052:	gap of unknown length
*	39053	40524:	contig of 1472 bp in length
*	40525	40624:	gap of unknown length
*	40625	42194:	contig of 1570 bp in length
*	42195	42294:	gap of unknown length
*	42295	43782:	contig of 1488 bp in length
*	43783	43882:	gap of unknown length
*	43883	45446:	contig of 1564 bp in length
*	45447	45546:	gap of unknown length
*	45547	46984:	contig of 1438 bp in length
*	46985	47084:	gap of unknown length
*	47085	48952:	contig of 1868 bp in length
*	48953	49052:	gap of unknown length
*	49053	50860:	contig of 1808 bp in length
*	50861	50960:	gap of unknown length
*	50961	52789:	contig of 1829 bp in length
*	52790	52889:	gap of unknown length
*	52890	55277:	contig of 2388 bp in length
*	55278	55377:	gap of unknown length
*	55378	56736:	contig of 1359 bp in length
*	56737	56836:	gap of unknown length
*	56837	58697:	contig of 1861 bp in length
*	58698	58797:	gap of unknown length
*	58798	60311:	contig of 1514 bp in length
*	60312	60411:	gap of unknown length
*	60412	62535:	contig of 2124 bp in length
*	62536	62635:	gap of unknown length
*	62636	64106:	contig of 1471 bp in length
*	64107	64206:	gap of unknown length
*	64207	66041:	contig of 1835 bp in length
*	66042	66141:	gap of unknown length
*	66142	68585:	contig of 2444 bp in length
*	68586	68685:	gap of unknown length
*	68686	71182:	contig of 2497 bp in length
*	71183	71282:	gap of unknown length
*	71283	73823:	contig of 2541 bp in length
*	73824	73923:	gap of unknown length
*	73924	76163:	contig of 2240 bp in length
*	76164	76263:	gap of unknown length
*	76264	78865:	contig of 2602 bp in length
*	78866	78965:	gap of unknown length
*	78966	80953:	contig of 1988 bp in length
*	80954	81053:	gap of unknown length
*	81054	83204:	contig of 2151 bp in length
*	83205	83304:	gap of unknown length
*	83305	85471:	contig of 2167 bp in length
*	85472	85571:	gap of unknown length
*	85572	88563:	contig of 2992 bp in length
*	88564	88663:	gap of unknown length
*	88664	91554:	contig of 2891 bp in length
*	91555	91654:	gap of unknown length
*	91655	94361:	contig of 2707 bp in length
*	94362	94461:	gap of unknown length
*	94462	99463:	contig of 5002 bp in length

Query Match	2.48;	Score 39;	DB 2;	Length 114558;
Best Local Similarity	100.08;	Pred. NO. 9e-11;		
Matches 39;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	333	ACACCTGAATTCACGGCCAATGAAGTTCGGAAAGTGAAC	371
Db	83890	ACACCTGAATTCACGGCCAATGAAGTTCGGAAAGTGAAC	83852

RESULT 34

LOCUS	AC129612	160331 bp	DNA	linear	HTG 24-AUG-2002
DEFINITION	Rattus norvegicus clone CH230-129J12, *** SEQUENCING IN PROGRESS				
	***, 65 unordered pieces.				

ACCESSION	AC129612
VERSION	AC129612.1
	GI:22024295

KEYWORDS
SOURCE
ORGANISM

HTG; HTGS_PHASE1.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 160331)
Muzny,D.,Marie., Metzker,M.,Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Andriano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,X., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Ditt,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Iduphird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,L., Lozado,R.J., Lu,K., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., Mcleod,M., McNeill,T., Meenen,E., Milosavljevic,A.,
Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
Newton,N., Nguyen,N., Norris,S., Nwaokemelehu,C., Okwuonu,G.,
Olarupunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A.,
Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quitoiz,J., Rachlin,E.,
Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Saverly,G., Scherer,S.,
Scott,G., Shatsman,S., Shen,H., Shetty,J., Shwartsbeyn,A.,
Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Schlegren,E.,
Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,
Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,K., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 160331)
Worley,K.C.

TITLE
JOURNAL

Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS

3 (bases 1 to 160331)
Rat Genome Sequencing Consortium.

TITLE
JOURNAL

Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KB2W
Center clone name: CH230-129J12
----- Summary Statistics
Sequencing vector: plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 92870 bases at least Q40
Consensus quality: 98530 bases at least Q30
Consensus quality: 102440 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1134 1133: contig of 1133 bp in length
1234 1233: gap of unknown length
1234 2370: contig of 1137 bp in length
2371 2470: gap of unknown length
2471 3498: contig of 1028 bp in length
3459 3598: gap of unknown length
3559 4613: contig of 1015 bp in length
4614 4713: gap of unknown length
4714 5767: contig of 1054 bp in length
5768 5867: gap of unknown length
5868 7351: contig of 1484 bp in length
7352 7451: gap of unknown length
7452 9083: contig of 1632 bp in length
9084 9183: gap of unknown length
9184 10473: contig of 1290 bp in length
10474 10573: gap of unknown length
10574 12180: contig of 1607 bp in length
12181 12280: gap of unknown length
12281 13424: contig of 1144 bp in length
13425 13524: gap of unknown length
13525 15050: contig of 1526 bp in length
15051 15150: gap of unknown length
15151 16168: contig of 1018 bp in length
16169 16268: gap of unknown length
16269 17904: contig of 1636 bp in length
17905 18004: gap of unknown length
18005 19034: contig of 1030 bp in length
19035 19134: gap of unknown length
19135 20213: contig of 1079 bp in length
20214 20313: gap of unknown length
20314 22122: contig of 1809 bp in length
22123 22222: gap of unknown length
22223 24159: contig of 1937 bp in length
24160 24259: gap of unknown length
24260 25660: contig of 1401 bp in length
25661 25760: gap of unknown length
25761 27102: contig of 1342 bp in length
27103 27202: gap of unknown length
27203 28639: contig of 1437 bp in length
28640 28739: gap of unknown length
28740 29939: contig of 1200 bp in length
29940 30039: gap of unknown length
30040 31055: contig of 1016 bp in length
31056 31155: gap of unknown length
31156 32505: contig of 1350 bp in length
32506 32605: gap of unknown length
32606 33930: contig of 1325 bp in length
33931 34030: gap of unknown length
34031 35352: contig of 1322 bp in length
35353 35452: gap of unknown length
35453 37015: contig of 1563 bp in length

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*	39631	39730:	gap of unknown length
*	39731	41572:	contig of 1842 bp in length
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*	41673	43363:	contig of 1691 bp in length
*	43364	43463:	gap of unknown length
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*	46254	47753:	contig of 1500 bp in length
*	47754	47853:	gap of unknown length
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*	49752	51191:	contig of 1440 bp in length
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*	51292	52673:	contig of 1382 bp in length
*	52674	52773:	gap of unknown length
*	52774	54972:	contig of 2199 bp in length
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*	55073	57153:	contig of 2081 bp in length
*	57154	57253:	gap of unknown length
*	57254	59614:	contig of 2361 bp in length
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*	59715	61186:	contig of 1472 bp in length
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*	64741	64840:	gap of unknown length
*	64841	66353:	contig of 1513 bp in length
*	66354	66453:	gap of unknown length
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*	68874	72002:	contig of 3129 bp in length
*	72003	72102:	gap of unknown length
*	72103	74179:	contig of 2077 bp in length
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*	74280	76076:	contig of 1797 bp in length
*	76077	76176:	gap of unknown length
*	76177	77703:	contig of 1527 bp in length
*	77704	77803:	gap of unknown length
*	77804	80423:	contig of 2620 bp in length
*	80424	80523:	gap of unknown length
*	80524	84110:	contig of 3587 bp in length
*	84111	84210:	gap of unknown length
*	84211	87326:	contig of 3116 bp in length
*	87327	87426:	gap of unknown length
*	87427	89863:	contig of 2437 bp in length
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Best Local Similarity 100.0%; Pred. No. 8.8e-11;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 ACACCTGAATTCAGGCCATGAGTTCGGAAGTGAAG 371
|||||
Db 156808 ACACCTGAATTCAGGCCATGAGTTCGGAAGTGAAG 156846

RESULT 35
LOCUS MMU89404 246 bp mRNA linear ROD 23-SEP-1998
DEFINITION Mus musculus strain BALB/c inosine-5'-monophosphate dehydrogenase 2
mRNA, partial cds.
ACCESSION U89404.1 GI:3642640
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
*REFERENCE
1 (bases 1 to 246)
AUTHORS Chu,C.C. and Paul,W.E.

TITLE Expressed genes in interleukin-4 treated B cells identified by cDNA
representational difference analysis
JOURNAL Mol. Immunol. 35 (8), 487-502 (1998)
MEDLINE 99012997
PUBMED 9798653
REFERENCE 2 (bases 1 to 246)
AUTHORS Chu,C.C. and Paul,W.E.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-1997) Lab. of Immunology, NIAID, Building 10,
Room 11N311, Bethesda, MD 20892-1892, USA
FEATURES
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/protein_id="AAC36511.1"
/db_xref="GI:3642641"
/translation="GQNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVYLACGRPOA
TAVYKVSEYARRFGVPVIADGCIQNVGHIAKALALGAF"
BASE COUNT 51 a 57 c 75 g 63 t
ORIGIN

Query Match 2.3%; Score 38; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1131 ATTGCTGATCGAGGAATCCAAATGTCGTCATATTGC 1168
|||||
Db 184 ATTGCTGATCGAGGAATCCAAATGTCGTCATATTGC 221

RESULT 36
LOCUS AC103220 168808 bp DNA linear HTG 13-JUL-2002
DEFINITION Rattus norvegicus clone CH230-48M6, *** SEQUENCING IN PROGRESS ***,
63 unordered pieces.
AC103220
AC103220.3 GI:21731183
VERSION
KEYWORDS HTG; HTGS_PHASE1.
SOURCE
ORGANISM

Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 168808)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarta,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs1,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,

Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Lune, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mel, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, A., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczkyk, R., Wooder, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

TITLE	Direct Submission
JOURNAL	unpublished
REFERENCE	2 (bases 1 to 168808)

TITLE	JOURNAL
Direct Submission	Submitted (24-NOV-2001)
Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
3 (bases 1 to 168808)	

TITLE	Direct Submission
JOURNAL	Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Jul 11, 2002 this sequence version replaced gi:17974711.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc.help@bcm.tmc.edu
----- Project Information

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/GenBank_draft_data.html)
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 63 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

*	1	1359:	contig of 1359 bp in length
*	1360	1459:	gap of unknown length
*	1460	2564:	contig of 1105 bp in length
*	2565	2664:	gap of unknown length
*	2665	4113:	contig of 1449 bp in length
*	4114	4213:	gap of unknown length
*	4214	5667:	contig of 1454 bp in length
*	5668	7479:	gap of unknown length
*	5768	7579:	contig of 1712 bp in length
*	7480	7579:	gap of unknown length
*	7580	8718:	contig of 1139 bp in length
*	8719	8818:	gap of unknown length

*	8819	10257:	contig of 1439 bp in length
*	10258	10357:	gap of unknown length
*	10358	11631:	contig of 1274 bp in length
*	11632	11731:	gap of unknown length
*	11732	13108:	contig of 1377 bp in length
*	13109	13208:	gap of unknown length
*	13209	14306:	contig of 1098 bp in length
*	14307	14406:	gap of unknown length
*	14407	15427:	contig of 1021 bp in length
*	15428	15527:	gap of unknown length
*	15528	16648:	contig of 1121 bp in length
*	16649	16748:	gap of unknown length
*	16749	19101:	contig of 2353 bp in length
*	19102	19201:	gap of unknown length
*	19202	21321:	contig of 2120 bp in length
*	21322	21421:	gap of unknown length
*	21422	23074:	contig of 1653 bp in length
*	23075	23174:	gap of unknown length
*	23175	24513:	contig of 1339 bp in length
*	24514	24613:	gap of unknown length
*	24614	25820:	contig of 1207 bp in length
*	25821	25920:	gap of unknown length
*	25921	27102:	contig of 1182 bp in length
*	27103	27202:	gap of unknown length
*	27203	28497:	contig of 1295 bp in length
*	28498	28597:	gap of unknown length
*	28598	30228:	contig of 1631 bp in length
*	30229	30328:	gap of unknown length
*	30329	31341:	contig of 1013 bp in length
*	31342	31441:	gap of unknown length
*	31442	33395:	contig of 1954 bp in length
*	33396	33495:	gap of unknown length
*	33496	34901:	contig of 1406 bp in length
*	34902	35001:	gap of unknown length
*	35002	37643:	contig of 2642 bp in length
*	37644	37743:	gap of unknown length
*	37744	39049:	contig of 1306 bp in length
*	39050	39149:	gap of unknown length
*	39150	40518:	contig of 1369 bp in length
*	40519	40618:	gap of unknown length
*	40619	42516:	contig of 1898 bp in length
*	42517	44169:	gap of unknown length
*	42617	44269:	gap of unknown length
*	44170	45701:	contig of 1432 bp in length
*	44270	45801:	gap of unknown length
*	45702	47590:	contig of 1789 bp in length
*	45802	47690:	gap of unknown length
*	47551	47690:	gap of unknown length
*	47651	48832:	contig of 1142 bp in length
*	48833	48932:	gap of unknown length
*	48933	51270:	contig of 2338 bp in length
*	51271	51370:	gap of unknown length
*	51371	53607:	contig of 2237 bp in length
*	53608	53707:	gap of unknown length
*	53708	56265:	contig of 2558 bp in length
*	56266	56365:	gap of unknown length
*	56366	59684:	contig of 3319 bp in length
*	59685	59784:	gap of unknown length
*	59785	61687:	contig of 1903 bp in length
*	61688	61787:	gap of unknown length
*	61788	63750:	contig of 1963 bp in length
*	63751	65650:	gap of unknown length
*	63851	65690:	contig of 1840 bp in length
*	65691	65790:	gap of unknown length
*	65791	69754:	contig of 3964 bp in length
*	69755	69854:	gap of unknown length
*	69855	71431:	contig of 1577 bp in length
*	71432	71531:	gap of unknown length
*	71532	74389:	contig of 2858 bp in length
*	74390	77489:	gap of unknown length
*	74490	77318:	contig of 2829 bp in length
*	77319	77418:	gap of unknown length
*	77419	80598:	contig of 3180 bp in length

* 80599: gap of unknown length
* 80699: contig of 2794 bp in length
* 83493: gap of unknown length
* 83593: contig of 4211 bp in length
* 87804: gap of unknown length
* 87904: contig of 3287 bp in length
* 91191: gap of unknown length
* 91291: contig of 3213 bp in length
* 94504: gap of unknown length
* 94604: contig of 3661 bp in length
* 98265: gap of unknown length
* 98365: contig of 3718 bp in length
* 102083: gap of unknown length
* 102183: contig of 4908 bp in length
* 107091: gap of unknown length
* 107191: contig of 4077 bp in length
* 111268: gap of unknown length
* 111368: contig of 4567 bp in length
* 115935: gap of unknown length
* 116035: contig of 3659 bp in length
* 119694: gap of unknown length
* 119794: contig of 5403 bp in length

Query Match 2.0%; Score 33; DB 2; Length 168808;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1335 TATTTTCAGTGAAGCTGACAAATCAAGTGCC 1367
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Db 75466 TATTTTCAGTGAAGCTGACAAATCAAGTGCC 75498

RESULT 37
LOCUS AR119642 44 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6153398.
ACCESSION AR119642
VERSION AR119642.1 GI:14102341
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Collart,F.R. and Huberman,E.
TITLE Method to identify specific inhibitors of IMP dehydrogenase
JOURNAL Patent: US 6153398-A 1 28-NOV-2000;
FEATURES
Source 1..44
BASE COUNT 11 a 10 c 13 g 10 t
ORIGIN

Query Match 1.8%; Score 30; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 ATGGCCGACTACCTGATTAGTGGGCACG 77
|||||
Db 15 ATGGCCGACTACCTGATTAGTGGGCACG 44

RESULT 38
LOCUS HUMYQ19A04 687 bp mRNA linear PRI 04-AUG-1998
DEFINITION Homo sapiens full length insert cDNA YQ19A04.
ACCESSION AF075074
VERSION AF075074.1 GI:3377615
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 687)

AUTHORS Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Marth,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
Giesel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L.,
Wilson,R. and Waterston,R.
TITLE Full Clone Sequencing of the Longest Available Member from Each
Unigene Cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 687)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No
attempt has been made to verify whether this corresponds to the
full-length of the original mRNA from which it was derived. We
have tried to obtain double-stranded, or double chemistry sequence
across the entire clone, but potentially, there are areas in the
sequence where this level of coverage was not achieved.
Nevertheless, we are confident of the accuracy of this sequence as
all regions of low quality, as defined by PHRAP (P. Green, in
preparation), were visually inspected and edited accordingly. The
consensus quality values for this sequence have been submitted
separately.

FEATURES
Source The location of this clone is unknown.
1..687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:274158"
/clone_lib="Soares_fetal_liver_spleen_1NFLS"
repeat_region 402..687
BASE COUNT 195 a 178 c 165 g 149 t
ORIGIN

Query Match 1.8%; Score 29; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1617 GTTTTTCATTAAGTTTGAAGA 1645
|||||
Db 2 GTTTTTCATTAAGTTTGAAGA 30

RESULT 39
LOCUS AX348472 6193 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 167 from Patent WO0202806.
ACCESSION AX348472
VERSION AX348472.1 GI:18614508
KEYWORDS
SOURCE Synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Method and nucleic acids for pharmacogenomic methylation analysis
JOURNAL Patent: WO 0202806-A 167 10-JAN-2002;
FEATURES
Source Epigenomics AG (DE)
1..6193
/organism="synthetic construct"

*	26270	26369: gap of unknown length
*	26370	27985: contig of 1616 bp in length
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*	28086	29407: contig of 1322 bp in length
*	29408	29507: gap of unknown length
*	29508	30634: contig of 1127 bp in length
*	30635	30734: gap of unknown length
*	30735	31927: contig of 1193 bp in length
*	31928	32027: gap of unknown length
*	32028	33335: contig of 1308 bp in length
*	33336	33435: gap of unknown length
*	33436	35511: contig of 2076 bp in length
*	35512	35611: gap of unknown length
*	35612	37208: contig of 1597 bp in length
*	37209	37308: gap of unknown length
*	37309	38952: contig of 1644 bp in length
*	38953	39052: gap of unknown length
*	39053	40524: contig of 1472 bp in length
*	40525	40624: gap of unknown length
*	40625	42194: contig of 1570 bp in length
*	42195	42294: gap of unknown length
*	42295	43782: contig of 1488 bp in length
*	43783	43882: gap of unknown length
*	43883	45446: contig of 1564 bp in length
*	45447	45546: gap of unknown length
*	46985	46984: contig of 1438 bp in length
*	47085	48952: contig of 1868 bp in length
*	48953	49052: gap of unknown length
*	49053	50860: contig of 1808 bp in length
*	50861	50960: gap of unknown length
*	50961	52789: contig of 1829 bp in length
*	52790	52889: gap of unknown length
*	52890	55277: contig of 2388 bp in length
*	55278	55377: gap of unknown length
*	55378	56736: contig of 1359 bp in length
*	56737	56836: gap of unknown length
*	56837	58697: contig of 1861 bp in length
*	58698	58797: gap of unknown length
*	58798	60311: contig of 1514 bp in length
*	60312	60411: gap of unknown length
*	60412	62535: contig of 2124 bp in length
*	62536	62635: gap of unknown length
*	62636	64106: contig of 1471 bp in length
*	64107	64206: gap of unknown length
*	64207	66041: contig of 1835 bp in length
*	66042	66141: gap of unknown length
*	66142	68585: contig of 2444 bp in length
*	68586	68685: gap of unknown length
*	71183	71182: contig of 2497 bp in length
*	71282	71282: gap of unknown length
*	71283	73823: contig of 2541 bp in length
*	73824	73923: gap of unknown length
*	73924	76163: contig of 2240 bp in length
*	76164	76263: gap of unknown length
*	76264	78865: contig of 2602 bp in length
*	78866	78965: gap of unknown length
*	78966	80953: contig of 1988 bp in length
*	80954	81053: gap of unknown length
*	81054	83204: contig of 2151 bp in length
*	83205	83304: gap of unknown length
*	83305	85471: contig of 2167 bp in length
*	85472	85571: gap of unknown length
*	85572	88563: contig of 2992 bp in length
*	88564	88663: gap of unknown length
*	88664	91554: contig of 2891 bp in length
*	91555	91654: gap of unknown length
*	91655	94361: contig of 2707 bp in length
*	94362	94461: gap of unknown length
*	94462	99463: contig of 5002 bp in length

Query Match 1.7%; Score 28; DB 2; Length 114558;
Best Local Similarity 100.0%; Pred. No. 0.00031;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1216 TGGCTGCCACCTGAGCCCCCTGTGA 1243
Db 49648 TGGCTGCCACCTGAGCCCCCTGTGA 49675

RESULT 41
AR119643/c
LOCUS AR119643 42 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6153398.
ACCESSION AR119643
VERSION AR119643.1 GI:14102342
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 42)
AUTHORS Collart,F.R. and Huberman,E.
TITLE Method to identify specific inhibitors of IMP dehydrogenase
JOURNAL Patent: US 6153398-A 2.28-NOV-2000;
FEATURES
source location/Qualifiers
1. .42
/organism="unknown"

BASE COUNT 15 a 10 c 7 g 10 t
ORIGIN

Query Match 1.6%; Score 26; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1568 TTCGTATGAGACGGCTTTCTGAA 1593
Db 42 TTCGTATGAGACGGCTTTCTGAA 17

RESULT 42
AX190187/c
LOCUS AX190187 50 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 366 from Patent WO0147942.
ACCESSION AX190187
VERSION AX190187.1 GI:15143563
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147942-A 366 05-JUL-2001;
Curagen Corporation (US)

FEATURES
source location/Qualifiers
1. .50
/organism="Homo sapiens"

/db_xref="taxon:9606"
/note="2 of 2 allelic variants (365 is other entry)"
misc_feature 25. .26
Accession number cg43922096"

BASE COUNT 12 a 20 c 12 g 6 t
ORIGIN

Query Match 1.6%; Score 26; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 CGGCGGTGCTGTGTGGCCATGGC 52
Db 50 CGGCGGTGCTGTGTGGCCATGGC 25

RESULT 43
AX190185/c
LOCUS AX190185 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 364 from Patent WO0147942.
ACCESSION AX190185
VERSION AX190185.1 GI:15143561
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147942-A 364 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (363 is other
entry)-Accession number cg43922096"
BASE COUNT 6 a 18 c 12 g 15 t
ORIGIN

Query Match 1.6%; Score 26; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 AGAGGAGACTTGGTGTAGCCCC 614
Db 51 AGAGCGAGACTTGGTGTAGCCCC 26

RESULT 44
AX418043/c
LOCUS AX418043 35 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 53 from Patent WO0185952.
ACCESSION AX418043
VERSION AX418043.1 GI:21523088
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Krystek,S.R., Sheriff,S., Witmer,M.R., Hollenbaugh,D.L., Yan,N.,
Mouravieff,J.E., Einspahr,H.M. and Kish,K.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and
uses thereof
JOURNAL Patent: WO 0185952-A 53 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source location/Qualifiers
1..35
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 10 a 9 c 7 g 9 t
ORIGIN

Query Match 1.5%; Score 25; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1570 CGTATGAGAGCGGCTTTCGAAA 1594
Db 35 CGTATGAGAGCGGCTTTCGAAA 11

RESULT 45
AX190184/c
LOCUS AX190184 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 363 from Patent WO0147942.

ACCESSION AX190184
VERSION AX190184.1 GI:15143560
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147942-A 363 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="1 of 2 allelic variants (364 is other
entry)-Accession number cg43922096"
BASE COUNT 7 a 18 c 11 g 15 t
ORIGIN

Query Match 1.5%; Score 25; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 AGAGGAGACTTGGTGTAGCCCC 613
Db 51 AGAGCGAGACTTGGTGTAGCCCC 27

RESULT 46
AX418042
LOCUS AX418042 33 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 52 from Patent WO0185952.
ACCESSION AX418042
VERSION AX418042.1 GI:21523087
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Krystek,S.R., Sheriff,S., Witmer,M.R., Hollenbaugh,D.L., Yan,N.,
Mouravieff,J.E., Einspahr,H.M. and Kish,K.
TITLE Modified inosine 5'-monophosphate dehydrogenase polypeptides and
uses thereof
JOURNAL Patent: WO 0185952-A 52 15-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source location/Qualifiers
1..33
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 7 a 8 c 9 g 9 t
ORIGIN

Query Match 1.5%; Score 24; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGGCCGACTACCTGATTAGTGGG 71
Db 10 ATGGCCGACTACCTGATTAGTGGG 33

RESULT 47
AX418045/c
LOCUS AX418045 30 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 55 from Patent WO0185952.
ACCESSION AX418045
VERSION AX418045.1 GI:21523090
KEYWORDS
SOURCE human.

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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE          Krystek,S.R., Sheriff,S., Witmer,M.R., Hollenbaugh,D.L., Yan,N.,
JOURNAL        Mouravieff,J.E., Einspahr,H.M. and Kish,K.
FEATURES       Modified inosine 5'-monophosphate dehydrogenase polypeptides and
SOURCE         uses thereof
               Patent: WO 0185952-A 55 15-NOV-2001;
               Bristol-Myers Squibb Co. (US)
               location/Qualifiers
               1. .30
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
BASE COUNT     5 a      8 c      4 g      13 t
ORIGIN

Query Match    1.4%; Score 23; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 GTTCGGAAGTGAGAAATATGA 379
Db      30 GTTCGGAAGTGAGAAATATGA 8

RESULT 48
AR141891 AR141891 344 bp DNA linear PAT 08-AUG-2001
LOCUS     Sequence 3 from patent US 6147194.
DEFINITION AR141891
ACCESSION  AR141891
VERSION    AR141891.1 GI:15101407
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 344)
AUTHORS   Collart,F.R. and Huberman,E.
TITLE     Eukaryotic IMPDH polynucleotide and antibody compositions
JOURNAL   Patent: US 6147194-A 3 14-NOV-2000;
FEATURES   Location/Qualifiers
SOURCE     1. .344
BASE COUNT 93 a      76 c      101 g      74 t
ORIGIN

Query Match    1.4%; Score 23; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      705 GCCATCATTTGCCCGGACAGACCT 727
Db      295 GCCATCATTTGCCCGGACAGACCT 317

RESULT 49
AR141892/c AR141892 344 bp DNA linear PAT 08-AUG-2001
LOCUS     Sequence 4 from patent US 6147194.
DEFINITION AR141892
ACCESSION  AR141892
VERSION    AR141892.1 GI:15101408
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 344)
AUTHORS   Collart,F.R. and Huberman,E.
TITLE     Eukaryotic IMPDH polynucleotide and antibody compositions
JOURNAL   Patent: US 6147194-A 4 14-NOV-2000;
FEATURES   Location/Qualifiers
SOURCE     1. .344
BASE COUNT 74 a      76 g      101 c      93 t
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ORIGIN

Query Match    1.4%; Score 23; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      705 GCCATCATTTGCCCGGACAGACCT 727
Db      50 GCCATCATTTGCCCGGACAGACCT 28

RESULT 50
I06573 I06573 344 bp DNA linear PAT 02-DEC-1994
LOCUS     Sequence 4 from Patent WO 9001545.
DEFINITION I06573
ACCESSION  I06573
VERSION    I06573.1 GI:589655
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 344)
AUTHORS   Collart,F.R. and Huberman,E.
TITLE     METHOD AND MATERIALS RELATING TO IMPDH AND GMP PRODUCTION
JOURNAL   Patent: WO 9001545-A 4 22-FEB-1990;
FEATURES   Location/Qualifiers
SOURCE     1. .344
BASE COUNT 93 a      76 c      101 g      74 t
ORIGIN

Query Match    1.4%; Score 23; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      705 GCCATCATTTGCCCGGACAGACCT 727
Db      295 GCCATCATTTGCCCGGACAGACCT 317
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Search completed: February 13, 2003, 01:05:35
Job time : 4980 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 19:26:45 : Search time 336 seconds
(without alignment updates/sec
11085.730 Mill

Title: US-09-846-637C-3
Perfect score: 1654
Sequence: 1 gaatcgggcggtcctcgga.....gtttagaaaaccggaattc 1654

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 470478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1438	86.9	1642	11 AAQ03540	Human IMPDH cDNA.
2	1127	68.1	2277	23 ABV29489	Human prostate exp
3	914	55.3	1677	23 ABV23631	Human prostate exp
4	914	55.3	1677	23 ABV24746	Human prostate exp
5	822	49.7	1157	24 ABK34910	Human CDNA encodin
6	783	47.3	1905	20 AA241300	Human normal ovari
7	662	40.0	2019	21 AAF21634	Human breast and o
8	615	37.2	1158	24 AAD28929	Human type II IMPD
9	613	37.1	1158	24 AAD28927	Human type II IMPD

10	612	37.0	1155	24 AAD28922	Human type II IMPD
11	612	37.0	1155	24 AAD28923	Human type II IMPD
12	612	37.0	1155	24 AAD28924	Human type II IMPD
13	612	37.0	1155	24 AAD28925	Human type II IMPD
14	612	37.0	1158	24 AAD28928	Human type II IMPD
15	410	24.3	674	21 AAF18367	Lung cancer associ
16	404	24.4	607	22 ABV44742	Human prostate exp
17	396	23.9	396	22 AAF94973	Human ovarian canc
18	396	23.9	396	24 ABT03240	Human ovarian carc
19	396	23.9	396	24 ABL48923	Ovarian carcinoma
20	361	21.3	554	21 AAC03976	Human secreted pro
21	296	17.9	420	23 ABV37312	Human prostate exp
22	283	17.1	675	21 AAZ80760	Human colon cancer
23	266	16.1	391	23 ABV07378	Human prostate exp
24	264	16.0	577	24 ABQ59475	Human colon cancer
25	242	14.5	6193	24 ABN95699	Gene #2197 used to
26	230	13.9	558	24 ABQ58310	Human colon cancer
27	209	12.5	10557	24 AAS18240	Human colon cancer
28	154	9.3	379	23 ABV14868	Reference sequence
29	153	9.3	437	23 ABV38955	Human prostate exp
30	112	6.8	389	23 ABV05699	Human prostate exp
31	69	4.2	286	22 AA184483	Human polynucleoti
32	62	3.7	1620	11 AAQ03541	Chinese hamster IM
33	60	3.6	60	24 ABN32859	Human spliced tran
34	51	3.1	51	22 AAH90485	Human clone cg4392
35	48	2.9	50	16 AAT25471	Human gene signatu
36	28	1.7	6193	22 ABK40085	Human chemically p
37	26	1.6	50	22 AAH90486	Human clone cg4392
38	26	1.6	51	22 AAH90484	Human clone cg4392
39	25	1.5	35	24 AAD28933	Human wild-type, t
40	25	1.5	51	22 AAH90483	Human clone cg4392
41	24	1.5	27	21 AAA30019	Hairpin hybridizer
42	24	1.5	29	21 AAA30020	Hairpin hybridizer
43	24	1.5	33	24 AAD28932	Human wild-type, t
44	23	1.4	23	21 AAA30021	Hairpin hybridizer
45	23	1.4	27	21 AAA30022	Hairpin hybridizer
46	23	1.4	29	21 AAA30006	Hairpin hybridizer
47	23	1.4	29	21 AAA30023	Hairpin hybridizer
48	23	1.4	30	24 AAD28935	Human type II DKT-
49	22	1.3	30	24 AAD28937	Human type II GSG-
50	22	1.3	33	24 AAD28939	Human type II AGRP

ALIGNMENTS

RESULT 1				
ID	AAQ03540	standard;	CDNA;	1642 BP.
AC	AAQ03540;			
XX				
DT	31-AUG-1990	(first entry)		
XX				
DE	Human IMPDH cDNA.			
XX				
KW	Inosine 5'-mono-phosphate dehydrogenase; hepatomas;			
KW	guanosine monophosphate; ss.			
XX				
OS	Homo sapiens.			
XX				
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FT		/product=Human IMPDH		
FT		1584..1586		
FT		/*tag= b		
FT		1..6		
FT		/*tag= c		
FT		/label=Box 1		
FT		19..26		
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FT		/label=Box 2		
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XX MO9001545-A.
PN
XX 22-FEB-1990.
PD
XX 02-AUG-1989; 89MO-0000344.
PF
XX
PR 12-AUG-1988; 88US-0232302.
XX
PA (ARCH-) ARCH. DEV. CORP.
XX
PI Collart FR, Huberman E;
XX
DR WPI; 1990-083504/11.
DR P-PSDB; AAR05432.
XX
PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
PT used to detect high levels of enzyme activity of tumour cells,
PT esp. hepatomas, and to produce guanosine monophosphate.
XX
PS Claim 8; Fig 1; 51pp; English.
XX
CC The sequence can be used to quantitatively detect IMPDH encoding
CC DNA or RNA by hybridisation, eg in normal and malignant cells,
CC esp. hepatomas.
CC See also AA003541.
XX
SQ Sequence 1642 BP; 411 A; 416 C; 449 G; 366 T; 0 other;

Query Match 86.9%; Score 1438; DB 11; Length 1642;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GGGCGTCTCGGAGACACGCGGCTGCTGTGTGGCCATGGCCGACTACCTGATTA 66
Db 1 GGGCGTCTCGGAGACACGCGGCTGCTGTGTGGCCATGGCCGACTACCTGATTA 60
QY 67 GTGGGGCACGTCCTACGATGTCAGACGAGGACTCACAGACAGCAGCTCTTCAACTGCG 126
Db 61 GTGGGGCACGTCCTACGATGTCAGACGAGGACTCACAGACAGCAGCTCTTCAACTGCG 120
QY 127 GAGACGGCCTCACATAGACTTCTCATCTCCCTGGGTACATCGACTTCACCTGCAG 186
Db 121 GAGACGGCCTCACATAGACTTCTCATCTCCCTGGGTACATCGACTTCACCTGCAG 180
QY 187 ACCAGGTGACCTGACTTCTGCTGTGACCAAGAAATCACTCTTAAGACCCCACTGTTT 246
Db 181 ACCAGGTGACCTGACTTCTGCTGTGACCAAGAAATCACTCTTAAGACCCCACTGTTT 240
QY 247 CCTCTCCCATGACACAGTACAGAGGCTGGGATGCCATAGCAATGGCGCTTACAGCGG 306
Db 241 CCTCTCCCATGACACAGTACAGAGGCTGGGATGCCATAGCAATGGCGCTTACAGCGG 300
QY 307 GTATTGGCTTCATCCACCACTGTACACCTGTAATTCAGGCCAATGAGTTGCGAAG 366
Db 301 GTATTGGCTTCATCCACCACTGTACACCTGTAATTCAGGCCAATGAGTTGCGAAG 360
QY 367 TGAAGAAATATGACAGGAGTTTCATCACAGACCCTGTGTCTCAGCCCAAGGATCGCG 426
Db 361 TGAAGAAATATGACAGGAGTTTCATCACAGACCCTGTGTCTCAGCCCAAGGATCGCG 420
QY 427 TCGGGGATGTTTTGAGGCCAAGGCCCGGATGTTTCTGCGGTATCCCAATCACAGACA 486
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QY 487 CAGGCCGGATGGGAGCCGCTTGTGGGCATCTCTCCAGGGAGCATGTTTCTCA 546
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QY 547 AAGAGGAGGAACATGACTGTTTCTTGAAGAGATAATGACAAAGAGGAGAACTTGTGG 606
Db 541 AAGAGGAGGAACATGACTGTTTCTTGAAGAGATAATGACAAAGAGGAGAACTTGTGG 600

QY 607 TAGCCCCCGCACGATCACACTGAAGGAGGCAAAATGAAATTCTGCAGCGCACAGAAAGG 666
Db 601 TAGCCCCCGCACGATCACACTGAAGGAGGCAAAATGAAATTCTGCAGCGCACAGAAAGG 660
QY 667 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGCCCATCATTTGCCGACAGACC 726
Db 661 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGCCCATCATTTGCCGACAGACC 720
QY 727 TGAAGAAGATCGGGACTTACCCTAGCCTCCAAAGATGCCAAGAACAGCTGCTGTGTG 786
Db 721 TGAAGAAGATCGGGACTTACCCTAGCCTCCAAAGATGCCAAGAACAGCTGCTGTGTG 780
QY 787 GGGCAGCCATTTGGCACTCATGAGGATGACAGTATAGGCTGGACTTGTGCCAGGCTG 846
Db 781 GGGCAGCCATTTGGCACTCATGAGGATGACAGTATAGGCTGGACTTGTGCCAGGCTG 840
QY 847 GTGTGATGTAGTGGTTTTTGGACTCTTCCAGGGAAATTCATCTTCCAGATCAATATGA 906
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QY 907 TCAAGTACATCAAGACAAATACCCTAATCTCCAAGTCAATTGGAGCAATGTGTCACCTG 966
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QY 1087 TGTACAAGGTGTATGAGTATGACAGCGCGCTTTGGTGTCCGGTCAATTGCTGATGGAGAA 1146
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QY 1207 GCTCTCTCTGCTGCCACCACTGAGGCCCTGTGTAATACTTCTTCCGATGGGATCC 1266
Db 1201 GCTCTCTCTGCTGCCACCACTGAGGCCCTGTGTAATACTTCTTCCGATGGGATCC 1260
QY 1267 GGCTAAAGAAATATCGCGGTATGGTTCCTCGATGCCATGACAAACCTCAGCAGCC 1326
Db 1261 GGCTAAAGAAATATCGCGGTATGGTTCCTCGATGCCATGACAAACCTCAGCAGCC 1320
QY 1327 AGACAGATATTTCAAGTGAAGCTGACAAAAATCAAAGTGGCCAGGGAGTGTCTGTGCTG 1386
Db 1321 AGACAGATATTTCAAGTGAAGCTGACAAAAATCAAAGTGGCCAGGGAGTGTCTGTGCTG 1380
QY 1387 TGCAGGACAAAGGGTCAATCCACAATTTGTCCCTTACCTGATTTGCTGGCATCCAACT 1446
Db 1381 TGCAGGACAAAGGGTCAATCCACAATTTGTCCCTTACCTGATTTGCTGGCATCCAACT 1440
QY 1447 CATGCCAGGACATTTGGTGCCAAAGAGCTTGACCCCAAGTCCGAGGCCATGATGTAATCTG 1506
Db 1441 CATGCCAGGACATTTGGTGCCAAAGAGCTTGACCCCAAGTCCGAGGCCATGATGTAATCTG 1500
QY 1507 AGCTTAAGTTTGAGAAGAGAAAGTCTCAGGCCAGGTGGAAGGTGGCTCCATAGCCTCC 1566
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QY 1567 ATTCGTATGAGAAGCGGCTTTTCTGAAGAAAGGATCCAGCACACCTCCGGTTTTTTTTT 1626
Db 1561 ATTCGTATGAGAAGCGGCTTTTCTGAAGAAAGGATCCAGCACACCTCCGGTTTTTTTTT 1620
QY 1627 CAATAAAGTTTGAAGAACCC 1648
Db 1621 CAATAAAGTTTGAAGAACCC 1642

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RESULT 2
ABV29489
ID   ABV29489 standard; cDNA; 2277 BP.
XX
AC   ABV29489;
XX
DT   16-SEP-2002 (first entry)
XX
DE   Human prostate expression marker cDNA 29480.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
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PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R, Endege WO, Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 6318; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ   Sequence 2277 BP; 644 A; 568 C; 653 G; 412 T; 0 other
Query Match          68.1%; Score 1127; DB 23; Length 2277;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1627; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY 189 CAGGTGACCTGACTTCTGCTGTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCC 248
DB 273 CAGGTGACCTGACTTCTGCTGTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCC 332
QY 249 TCTCCCATGACACAGTCCACAGAGGCTGGGATGGCCATAGCAATGGCGCTTACAGCGGT 308
DB 333 TCTCCCATGACACAGTCCACAGAGGCTGGGATGGCCATAGCAATGGCGCTTACAGCGGT 392
QY 309 ATTGGCTTCATCCACCACCACTGTACACCTGAATTCCAGGCCAATGAAGTTCCGAAGTG 368
DB 393 ATTGGCTTCATCCACCACCACTGTACACCTGAATTCCAGGCCAATGAAGTTCCGAAGTG 452
QY 369 AAGAATATGAAACAGGGATTTCATCACAGACCCTGTGTCCTCAGCCCCCAAGGATCGCGTG 428
DB 453 AAGAATATGAAACAGGGATTTCATCACAGACCCTGTGTCCTCAGCCCCCAAGGATCGCGTG 512
QY 429 CGGATGTTTTTGAGGCCAAGGCCCGGATGTTTCTGCGGTATCCCAATCACAGACACA 488
DB 513 CGGATGTTTTTGAGGCCAAGGCCCGGATGTTTCTGCGGTATCCCAATCACAGACACA 572
QY 489 GGCCGATGGGGAGCCGCTTGGTGGCATCATCTCCTCCAGGACATTTGATTTCTCAA 548
DB 573 GGCCGATGGGGAGCCGCTTGGTGGCATCATCTCCTCCAGGACATTTGATTTCTCAA 632
QY 549 GAGAGGAACATGACTGTTTCTTGAAGAGATTAATGACAAAGAGGGAAGACTTGTGTA 608
DB 633 GAGAGGAACATGACTGTTTCTTGAAGAGATTAATGACAAAGAGGGAAGACTTGTGTA 692
QY 609 GCCCCCGGACATCACACTGAAGGAGCAAAATGAATTTCTGACGGCAGCAAGAAGGA 668
DB 693 GCCCCCGGACATCACACTGAAGGAGCAAAATGAATTTCTGACGGCAGCAAGAAGGA 752
QY 669 AAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCGACAGACCTG 728
DB 753 AAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCGACAGACCTG 812
QY 729 AAGAAGATCGGGACTACCCACTAGCCTCCAAAGATGCCAAGAACAGCTGCTGTGGG 788
DB 813 AAGAAGATCGGGACTACCCACTAGCCTCCAAAGATGCCAAGAACAGCTGCTGTGGG 872
QY 789 GCAGCATTCGCATCATGAGATGACAGTATAGGCTGACCTGCAGCCAGGCTGCT 848
DB 873 GCAGCATTCGCATCATGAGATGACAGTATAGGCTGACCTGCAGCCAGGCTGCT 932
QY 849 GTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGATC 908
DB 933 GTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGATC 992
QY 909 AAGTACATCAAGACAATACCCTAATCTCCAAGTCATTTGAGGCAATGTGTCACCTGCT 968
DB 993 AAGTACATCAAGACAATACCCTAATCTCCAAGTCATTTGAGGCAATGTGTCACCTGCT 1052
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DB 1053 GCCCAGGCCAAGAACCTCATTTGATGACAGGTGTGATGCCCTGCGGCTGGGCATGGAAAT 1112
QY 1029 GGCTCCATTCGATTTATCCAGGAAGTGTGCTGTGGCGGCCCAAGCAACAGCAGTG 1088
DB 1113 GGCTCCATTCGATTTATCCAGGAAGTGTGCTGTGGCGGCCCAAGCAACAGCAGTG 1172
QY 1089 TACAAGGTATAGATATGACAGCGCTTGTGTTCCGTTGATTTGATGGAGAATC 1148
DB 1173 TACAAGGTATAGATATGACAGCGCTTGTGTTCCGTTGATTTGATGGAGAATC 1232
QY 1149 CAAAATGTGGTCATATTTGGAAGCCTTGCCCTTGCGGCTCCACAGTCATGATGGGC 1208
DB 1233 CAAAATGTGGTCATATTTGGAAGCCTTGCCCTTGCGGCTCCACAGTCATGATGGGC 1292
QY 1209 TCTCTCTGCTGCTCAGCAGCACTGAGGCCCTGTGTAATACTTCTTTCCGATGGATCGGG 1268
DB 1293 TCTCTCTGCTGCTCAGCAGCACTGAGGCCCTGTGTAATACTTCTTTCCGATGGATCGGG 1352
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QY	1269	CTAAGAATATATCGCGGSTATGGGTCTCTCCGATGCCATGGACAAGCACCTTCAGCAGCCAG	1328
Db	1353	CTAAAGAAATATCGCGGTAATGGGTCTCTCGATGCCATGGACAAGCACCTTCAGCAGCCAG	1412
QY	1329	AACAGATATTTCAGTGAAGCTGCACAAAATCAAGTGCCCCAGGGAGTGTCTGTGCTGTG	1388
Db	1413	AACAGATATTTCAGTGAAGCTGCACAAAATCAAGTGCCCCAGGGAGTGTCTGTGCTGTG	1472
QY	1389	CAGGACAAAGGGTCAATCCACAATTTGTCCCCTTAACCTGATTGCTGGCATCCAACACTCA	1448
Db	1473	CAGGACAAAGGGTCAATCCACAATTTGTCCCCTTAACCTGATTGCTGGCATCCAACACTCA	1532
QY	1449	TGCCAGGACATTGGTGCCCAAGAGCTTGACCACAAGTCCGAGCCATGATGTACTCTGGGGAG	1508
Db	1533	TGCCAGGACATTGGTGCCCAAGAGCTTGACCACAAGTCCGAGCCATGATGTACTCTGGGGAG	1592
QY	1509	CTTAAAGTTTGAGAAGAGAACGTCCTCAGCCCAGGTGGAAGGTGGCTCCATAGCCTCCAT	1568
Db	1593	CTTAAAGTTTGAGAAGAGAACGTCCTCAGCCCAGGTGGAAGGTGGCTCCATAGCCTCCAT	1652
QY	1569	TCGTATGAGAAGCGGCTTTTCTGAAAAGGGATCCAGCACACCTCCTCGGTTTTTTTTTCA	1628
Db	1653	TCGTATGAGAAGCGGCTTTTCTGAAAAGGGATCCAGCACACCTCCTCGGTTTTTTTTTCA	1712
QY	1629	ATAAAAGTTTAGAAGA	1645
Db	1713	ATAAAAGTTTAGAAGA	1729

```

RESULT 3
ABV23631
ID ABV23631 standard; cDNA; 1677 BP.
XX
AC ABV23631;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 23622.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
OS
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 4329; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;

```

CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 1677 BP; 428 A; 446 C; 445 G; 358 T; 0 other;

	Query Match	55.3%;	Score 914;	DB 23;	Length 1677;	
	Best Local Similarity	99.3%;	Pred. No. 0;			
	Matches 1364;	Conservative	0;	Mismatches	9;	Indels 0; Gaps 0;
QY	187 ACCAGGTGACCTGACTTCTGCTCTGACCAGAATAATCACTTTAAGACCCCACTGGTTT					246
Db	132 ACCAGGTGACCTGACTTCTGCTCTGACCAGAATAATCACTTTAAGACCCCACTGGTTT					191
QY	247 CCTCTCCCATGGACACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGTTACAGCG					306
Db	192 CCTCTCCCATGGACACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGTTACAGCG					251
QY	307 GTATTGGCTTCATCCACCACAACCTGTACACCTGAATTCCAGGCCAATGAAGTTCGAAAG					366
Db	252 GTATTGGCTTCATCCACCACAACCTGTACACCTGAATTCCAGGCCAATGAAGTTCGAAAG					311
QY	367 TGAAGAATAATGAACAGGAGATTATCACAGACCCCTGTGGTCTCAGCCCCAAGGATCGCG					426
Db	312 TGAAGAATAATGAACAGGAGATTATCACAGACCCCTGTGGTCTCAGCCCCAAGGATCGCG					371
QY	427 TGCCGGATGTTTTTGAGGCCCAAGGCCCGGCATGGTTTCTGCGGTATCCCAATCACAGACA					486
Db	372 TGCCGGATGTTTTTGAGGCCCAAGGCCCGGCATGGTTTCTGCGGTATCCCAATCACAGACA					431
QY	487 CAGGCCGGATGGGAGAGCCGCTTGGTGGGCATCATCTCCTCAGGGACATTGATTTTCTCA					546
Db	432 CAGGCCGGATGGGAGAGCCGCTTGGTGGGCATCATCTCCTCAGGGACATTGATTTTCTCA					491
QY	547 AAGAGGAGGAACATGACTGTTTCTTGGAAAGAGATAATGACAAAGAGGGAAGACTTGGTGG					606
Db	492 AAGAGGAGGAACATGACTGTTTCTTGGAAAGAGATAATGACAAAGAGGGAAGACTTGGTGG					551
QY	607 TAGCCCCCGCAGCATCACACTGAAGGAGGCAAAATGAAAATCTGCAGCGCAGCAAGAAG					666
Db	552 TAGCCCCCGCAGCATCACACTGAAGGAGGCAAAATGAAAATCTGCAGCGCAGCAAGAAG					611
QY	667 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGACC					726
Db	612 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGACC					671
QY	727 TGAAGAAGAATCGGGACTACCCCACTAGCCTCCAAGATGCCAAGAAACAGCTGCTGTGTG					786
Db	672 TGAAGAAGAATCGGGACTACCCCACTAGCCTCCAAGATGCCAAGAAACAGCTGCTGTGTG					731
QY	787 GGGCAGCCATTTGGCAGTCATGAGGATGACAAGTATAGGCTGAGCTGTGCGCCAGGCTG					846
Db	732 GGGCAGCCATTTGGCAGTCATGAGGATGACAAGTATAGGCTGAGCTGTGCGCCAGGCTG					791
QY	847 GTGTGATGTAGTGGTTTTGGACTCTTCCCAGGGAATTCATCTTCCAGATCAATATGA					906
Db	792 GTGTGATGTAGTGGTTTTGGACTCTTCCCAGGGAATTCATCTTCCAGATCAATATGA					851
QY	907 TCAAGTACATCAAGACAATACCCCTAATCTCCAGTCAATTGGAGGCAATGTGTCAC TG					966
Db	852 TCAAGTACATCAAGACAATACCCCTAATCTCCAGTCAATTGGAGGCAATGTGTCAC TG					911
QY	967 CTGCCCAAGGCCAAGAACCTCATTTGATGCAGGTGTGGATGCCCTGCCGGTGGGCATGGCAA					1026
Db	912 CTGCCCAAGGCCAAGAACCTCATTTGATGCAGGTGTGGATGCCCTGCCGGTGGGCATGGCAA					971

QY	1027	GTGGCTCCATCTGCATTAATCCAGAGTGTGGCCCTGTGGCGGCC	AAGCAACAGCAG	1086
Db	972	GTGGCTCCATCTGCATTAACGACAGAGTGTGGCCCTGTGGCGGCC	AAGCAACAGCAG	1031
QY	1087	TGTACAAGGTGTATGAGTATGACACGGCGCTTGGTGTCCGGTCATT	CTGATGAGGAA	1146
Db	1032	TGTACAAGGTGTACAGATATGCACGGCGCTTGGTGTCCGGTCATT	CTGATGAGGAA	1091
QY	1147	TCCAAATATGGGTATATTTGCCGAAGCCTTGGCCCTTGGGGCCTCC	CAGTCATGATGG	1206
Db	1092	TCCAAATATGGGTATATTTGCCGAAGCCTTGGCCCTTGGGGCCTCC	CAGTCATGATGG	1151
QY	1207	GCTCTCTCCGTGGTGCACCCACTGAGGCCCTGGTGAATACTTCTTT	CCGATGGGATCC	1266
Db	1152	GCTCTCTCCGTGGTGCACCCACTGAGGCCCTGGTGAATACTTCTTT	CCGATGGGATCC	1211
QY	1267	GGCTAAGAATAATCGCGGTATGGTCTCTCGATGCCATGACACAAG	ACCTCAGCAGCC	1326
Db	1212	GGCTAAGAATAATCGCGGTATGGTCTCTCGATGCCATGACACAAG	ACCTCAGCAGCC	1271
QY	1327	AGAACAGATATTTCACTGAAGCTGACAAATCAAAAGTGGCCAGGAG	TGTCTGTGCTG	1386
Db	1272	AGAACAGATATTTCACTGAAGCTGACAAATCAAAAGTGGCCAGGAG	TGTCTGTGCTG	1331
QY	1387	TGCAGAGCAAAAGGTTCAATCCACAATTTGTCCCTTACCTGATTTGCT	GCATCCCAACACT	1446
Db	1332	TGCAGAGCAAAAGGTTCAATCCACAATTTGTCCCTTACCTGATTTGCT	GCATCCCAACACT	1391
QY	1447	CATGCCAGACATTTGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATG	TGTACTCTGGGG	1506
Db	1392	CATGCCAGACATTTGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATG	TGTACTCTGGGG	1451
QY	1507	AGCTTAAGTTTGAGAAGAGAACGTCCTCAGCCCAAGTGAAGTGGCG	TCCAT	1559
Db	1452	AGCTTAAGTTTGAGAAGAGAACGTCCTCAGCCCAAGTGAAGTGGCG	TCCAT	1504
RESULT 4				
ID	ABV24746			
XX	ABV24746 standard; cDNA; 1677 BP.			
AC	ABV24746;			
DT	16-SEP-2002 (first entry)			
DE	Human prostate expression marker cDNA 24737.			
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker			
KW	pharmacogenomic marker; gene; ss.			
OS	Homo sapiens.			
PN	WO200160860-A2.			
PD	23-AUG-2001.			
PF	20-FEB-2001; 2001WO-US05171.			
PR	17-FEB-2000; 2000US-183319P.			
PR	16-MAR-2000; 2000US-189862P.			
PR	25-MAY-2000; 2000US-207454P.			
PR	09-JUN-2000; 2000US-211314P.			
PR	18-JUL-2000; 2000US-219007P.			
PR	13-DEC-2000; 2000US-255281P.			
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.			
PI	Schlegel R, Endege WO, Monahan JE;			
RR	WPI; 2001-662795/76.			
TT	Novel isolated nucleic acid molecule associated with cancerous state of			

PT	prostate cells and correlating with presence of prostate cancer, useful									
PT	for detecting presence of prostate cancer, stage of prostate cancer									
XX										
PS	Claim 1; Page 4726; 11750bp; English.									
XX										
CC	The invention relates to an isolated nucleic acid molecule (I) comprising									
CC	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the									
CC	specification or its complement. (I) is useful for:									
CC	(a) assessing whether a patient is afflicted with prostate cancer;									
CC	(b) monitoring the progression of prostate cancer in a patient;									
CC	(c) assessing the efficacy of a test compound to inhibit prostate									
CC	cancer in a patient;									
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer									
CC	in a patient;									
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;									
CC	(f) assessing the prostate cell carcinogenic potential of a compound;									
CC	(g) determining whether prostate cancer has metastasized in a patient;									
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a									
CC	patient;									
CC	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.									
CC										
XX										
SO	Sequence 1677 BP; 428 A; 446 C; 445 G; 358 T; 0 other;									
Query Match 55.3%; Score 914; DB 23; Length 1677;										
Best Local Similarity 99.3%; Pred. No. 0;										
Matches 1364; Conservative 0; Mismatches 9; Indels 0; Gaps 0;										
QY	187	ACCAGGTGACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTT	246							
Db	132	ACCAGGTGACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTT	191							
QY	247	CCTCTCCCATGGACACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGTTACAGGCG	306							
Db	192	CCTCTCCCATGGACACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGTTACAGGCG	251							
QY	307	GTATTGGCTTCATCCACCACCACTGTACACCTGAAATTCAGGCCAATGAAGTTGCGAAAG	366							
Db	252	GTATTGGCTTCATCCACCACCACTGTACACCTGAAATTCAGGCCAATGAAGTTGCGAAAG	311							
QY	367	TGAAGAAATATGACACAGGGATTTCATCACAGACCTGTGGTCTCAGGCCCAAGATCGCG	426							
Db	312	TGAAGAAATATGACACAGGGATTTCATCACAGACCTGTGGTCTCAGGCCCAAGATCGCG	371							
QY	427	TGCGGATGTTTTTGTAGGCCAAGGCCCGCATGTTTTCTGCGGTATCCCAATCACAGACA	486							
Db	372	TGCGGATGTTTTTGTAGGCCAAGGCCCGCATGTTTTCTGCGGTATCCCAATCACAGACA	431							
QY	487	CAGGCCGATGGGAGCCGCTTGGTGGCATCATCTCTCCAGGGACATTTGATTTTCTCA	546							
Db	432	CAGGCCGATGGGAGCCGCTTGGTGGCATCATCTCTCCAGGGACATTTGATTTTCTCA	491							
QY	547	AAGAGGAGACATGACTGTTTCTTGAAGACAGATTAATGACAAAGAGGGAAGACTTGGTGG	606							
Db	492	AAGAGGAGACATGACTGTTTCTTGAAGACAGATTAATGACAAAGAGGGAAGACTTGGTGG	551							
QY	607	TAGCCCCCGCAGCATCACACTGAAGAGGCAATGAAATTTCTGACGCCGACCAAGAAGG	666							
Db	552	TAGCCCCCGCAGCATCACACTGAAGAGGCAATGAAATTTCTGACGCCGACCAAGAAGG	611							
QY	667	GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGGCCATCATTTGCCCGACAGACC	726							
Db	612	GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGGCCATCATTTGCCCGACAGACC	671							
QY	727	TGAAGAAGATCGGGACTACCCACTAGCCTTCCAAAGATGCCAAGAAGACAGCTGCTGTGTG	786							
Db	672	TGAAGAAGATCGGGACTACCCACTAGCCTTCCAAAGATGCCAAGAAGACAGCTGCTGTGTG	731							
QY	787	GGGACGCCATTGGCACTCATGAGGATGACACAGTATAGGCTGGACTTGGCTGCGCCAGGCTG	846							
Db	732	GGGACGCCATTGGCACTCATGAGGATGACACAGTATAGGCTGGACTTGGCTGCGCCAGGCTG	791							
QY	847	GTGTGATGTAGTGGTTTTGGACTCTTCCCGAGGAATTCATCTTCCAGATCATATATGA	906							

Db	792	GTGTGATGTAGTGGTTTGGACTCTTCCAGGAAATTCCATCTTCCAGATCATATGA	851
QY	907	TCAAGTACATCAAGACAATAATCCCTAATCTCCAAGTCAATTGGAGGCAATGTGTCAC	966
Db	852	TCAAGTACATCAAGACAATAATCCCTAATCTCCAAGTCAATTGGAGGCAATGTGTCAC	911
QY	967	CTGCCAGGCCAAGAACCTCATTTGATGCAGGTGAGTGCCTGCGGGTGGGCATGGGAA	1026
Db	912	CTGCCAGGCCAAGAACCTCATTTGATGCAGGTGAGTGCCTGCGGGTGGGCATGGGAA	971
QY	1027	GTGGCTCCATCTGCATTTATCCAGGAAGTGTGGCCTGTGGCGGCCCAAGCAACAGCAG	1086
Db	972	GTGGCTCCATCTGCATTTACGCAGAGAGTGTGGCCTGTGGCGGCCCAAGCAACAGCAG	1031
QY	1087	TGTACAAGTGTAATGATATGCACGGCGCTTGGTGTCCGGTCATTTGCTGATGCAGGAA	1146
Db	1032	TGTACAAGTGTAATGATATGCACGGCGCTTGGTGTCCGGTCATTTGCTGATGCAGGAA	1091
QY	1147	TCCAAATATGGGTCAATATTCGGAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGG	1206
Db	1092	TCCAAATATGGGTCAATATTCGGAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGG	1151
QY	1207	GCTCTCTCTGGGTGCCACCACCTGAGGCCCTGGTGAATACTCTTTTCCGATGGGATCC	1266
Db	1152	GCTCTCTCTGGGTGCCACCACCTGAGGCCCTGGTGAATACTCTTTTCCGATGGGATCC	1211
QY	1267	GGCTAAGAATAATCCGGTATGGGTTCTCTGATGCCATGACAAAGCACCTCAGCAGCC	1326
Db	1212	GGCTAAGAATAATCCGGTATGGGTTCTCTGATGCCATGACAAAGCACCTCAGCAGCC	1271
QY	1327	AGAACAGATATTCAGTGAAGCTGACAAAATCAAGTGCCCGCAGGAGTGCTGTGCTG	1386
Db	1272	AGAACAGATATTCAGTGAAGCTGACAAAATCAAGTGCCCGCAGGAGTGCTGTGCTG	1331
QY	1387	TGCAGGACAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGCATCCACACT	1446
Db	1332	TGCAGGACAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGCATCCACACT	1391
QY	1447	CATGCCAGACATTTGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATTTACTCTGGG	1506
Db	1392	CATGCCAGACATTTGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATTTACTCTGGG	1451
QY	1507	AGCTTAAGTTTGAGAGAAGAACGTCCTCAGCCGAGGTGGAAGGTGGCGTCCAT	1559
Db	1452	AGCTTAAGTTTGAGAGAAGAACGTCCTCAGCCGAGGTGGAAGGTGGCGTCCAT	1504
RESULT 5			
ID	ABK34910	standard; cDNA; 1157 BP.	
XX	ABK34910;		
AC	ABK34910;		
XX	08-MAY-2002	(first entry)	
DT	08-MAY-2002	(first entry)	
XX	Human cDNA encoding secreted protein #48.		
XX	Human; secreted protein; gene; ss: nutritional supplement; haemophilia;		
KW	viral infection; bacterial infection; fungal infection; diabetes; asthma;		
KW	autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;		
KW	autoimmune thyroiditis; allergic reaction; neurodegenerative disease;		
KW	Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;		
KW	coagulation disorder; inflammatory disorder; Crohn's disease; incision;		
KW	tissue regeneration; wound healing; burn; haematopoiesis;		
KW	myeloid cell deficiency; lymphoid cell deficiency.		
OS	Homo sapiens.		
XX	WO200177288-A2.		
PN	18-OCT-2001.		
XX	29-MAR-2001; 2001WO-US10224.		
PD			
XX			
PF			

XX	06-APR-2000; 2000US-195582P.		
PR	(GEMV) GENETICS INST INC.		
XX	Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;		
PI	Gulukota K, Graham JR;		
PI	WPI; 2002-179321/23.		
XX	Five hundred and ninety two polynucleotides derived from a variety of		
PT	human tissue sources which encode secreted proteins, useful for		
PT	treating immune deficiencies and disorders such as autoimmune disorders		
PT			
XX	Claim 1; Page 93; 372pp; English.		
PS	The invention relates to 592 polynucleotides which have been derived from		
CC	a variety of human tissue sources and which encode novel secreted		
CC	proteins. The polynucleotides can be used as probes for the		
CC	identification and isolation of full length cDNA and genomic DNA. The		
CC	polynucleotides and proteins can also be used as nutritional supplements.		
CC	The proteins are useful in the treatment of various immune deficiencies		
CC	and disorders such as viral infections, bacterial infections, fungal		
CC	infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple		
CC	sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions		
CC	and conditions (e.g. asthma). They are also useful for treating		
CC	neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's		
CC	disease), liver fibrosis, coagulation disorders (e.g. haemophilia),		
CC	inflammatory disorders (e.g. Crohn's disease) and tumours. They are also		
CC	useful for tissue regeneration, for wound healing and in the treatment of		
CC	burns, incisions and ulcers. The proteins are also useful for regulating		
CC	haematopoiesis and for treating myeloid or lymphoid cell deficiencies.		
CC	Sequences ABK34863-ABK35454 represent polynucleotides of the invention.		
XX	Sequence 1157 BP; 297 A; 270 C; 326 G; 264 T; 0 other;		
SQ			
Query Match			
Best Local Similarity 49.7%; Score 822; DB 24; Length 1157;			
Matches 1022; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	619	GCATCACACTGAAGGAGGCAAAATGAATTTCTGCAGCGCAGCAAGAAGGAAAGTTGCCCA	678
Db	131	GCATCACACTGAAGGAGGCAAAATGAATTTCTGCAGCGCAGCAAGAAGGAAAGTTGCCCA	190
QY	679	TTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGACAGACCTGAAGAAGATC	738
Db	191	TTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGACAGACCTGAAGAAGATC	250
QY	739	GGGACTACCCACTAGCCTCCAAAGATGCCAAGAACACAGCTGCTGTGTGGGGCAGCCATTG	798
Db	251	GGGACTACCCACTAGCCTCCAAAGATGCCAAGAACACAGCTGCTGTGTGGGGCAGCCATTG	310
QY	799	GCACTCATGAGATGACAAGTATAGGCTGCACTTGCTGCCCAGGCTGGTGTGATGTAG	858
Db	311	GCACTCATGAGATGACAAGTATAGGCTGCACTTGCTGCCCAGGCTGGTGTGATGTAG	370
QY	859	TGGTTTGGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGATCAAGTACATCA	918
Db	371	TGGTTTGGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGATCAAGTACATCA	430
QY	919	AAGACAATATCCCTAATCTCCAAGTCAATTTGAGGCAATGTGTCACCTGCCAGGCCA	978
Db	431	AAGACAATATCCCTAATCTCCAAGTCAATTTGAGGCAATGTGTCACCTGCCAGGCCA	490
QY	979	AGAACCCTCATTTGATGACAGGTGTGATGCCCTGGCGGGTGGGCATGGGAAGTGCTCATCT	1038
Db	491	AGAACCCTCATTTGATGACAGGTGTGATGCCCTGGCGGGTGGGCATGGGAAGTGCTCATCT	550
QY	1039	GCAATTATCCAGGAAGTGTGCTGTGGCGGCCCAAGCAACAGCAGTGTACAAGGTGT	1098
Db	551	GCAATTATCCAGGAAGTGTGCTGTGGCGGCCCAAGCAACAGCAGTGTACAAGGTGT	610

QY	1099	ATGAGTATGCACGGCGCTTTGGTGTGTCCGGTCATTCGTGATGGAGGA	TCCAAAATGTGG	1158
Db	611	CAGAGTATGCACGGCGCTTTGGTGTTCGGGTCAATTCGTATGGAGGA	TCCAAAATGTGG	670
QY	1159	GTCATATTGGCAAGGCTTGGCCCTTGGGGCCCTCAGCATGATG	GGCTCTCTCTGG	1218
Db	671	GTCATATTGGCAAGGCTTGGCCCTTGGGGCCCTCAGCATGATG	GGCTCTCTCTGG	730
QY	1219	CTGCCACCACTGAGGCCCTGGTGAATACTCTTTCCGATGGGATC	GGCTAAAGAAAT	1278
Db	731	CTGCCACCACTGAGGCCCTGGTGAATACTCTTTCCGATGGGATC	GGCTAAAGAAAT	790
QY	1279	ATCGCGGTATGGGTCTCTCGATGCCATGAGCAAGCACTCAGCAGC	AGAACAGATATT	1338
Db	791	ATCGCGGTATGGGTCTCTCGATGCCATGAGCAAGCACTCAGCAGC	AGAACAGATATT	850
QY	1339	TCAGTGAAGCTGACAAAATCAAAGTGGCCAGGAGTGTCTGGTCT	TTGCAGAGCAAAAG	1398
Db	851	TCAGTGAAGCTGACAAAATCAAAGTGGCCAGGAGTGTCTGGTCT	TTGCAGAGCAAAAG	910
QY	1399	GCTCAATCCACAAAATTTGTCCCTTACCTGATTGCTGGCATCCAAACAC	CATGCCAGGACA	1458
Db	911	GCTCAATCCACAAAATTTGTCCCTTACCTGATTGCTGGCATCCAAACAC	CATGCCAGGACA	970
QY	1459	TTGGTGCCAAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGG	AGCTTAAGTTTG	1518
Db	971	TTGGTGCCAAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGG	AGCTTAAGTTTG	1030
QY	1519	AGAAGAGAACGTCCTTCAGCCCAAGGTGGAAGGTGGCGTCCATAGCCTC	CAATTCGATGAGA	1578
Db	1031	AGAAGAGAACGTCCTTCAGCCCAAGGTGGAAGGTGGCGTCCATAGCCTC	CAATTCGATGAGA	1090
QY	1579	AGCGGCTTTTCTGA AAAAGGATCCAGCACACCTCTCGGTTTTTTT	CAATAAAAGTTT	1638
Db	1091	AGCGGCTTTTCTGA AAAAGGATCCAGCACACCTCTCGGTTTTTTT	CAATAAAAGTTT	1150
QY	1639	AGAAAG 1644		
Db	1151	AGAAAG 1156		

RESULT 6
AAZ41300
ID AAZ41300 standard; cDNA; 1905 BP.
XX
AC AAZ41300;
XX
DT 18-JAN-2000 (first entry)
XX
DE Human normal ovarian tissue derived cDNA 79.
XX
KW Human; ovary; screening; ovarian cancer; treatment; ss.
XX
OS Homo sapiens.
XX
PN DE19816395-A1.
XX
PD 07-OCT-1999.
XX
PF 03-APR-1998; 98DE-1016395.
XX
PR 03-APR-1998; 98DE-1016395.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilsarsky C, Dahl E;
XX
DR WPI; 1999-552352/47.
XX
PT Nucleic acid sequences potentially useful in diagnosis or therapy of
XX ovarian cancer -
PS Claim 3; Page 190; 274ppp; German.

XX This invention describes novel nucleic acid sequences that are highly
CC expressed in normal ovary tissue. Artificial chromosomes and cosmid
CC clones containing the sequences can be used as gene transfer vehicles.
CC The sequences can be used to produce DNA fragments containing
CC full-length genes. Host cells transformed with the sequences can be used
CC to produce polypeptides or polypeptide fragments, which can be used to
CC screen phage displays for polypeptides that bind to them, or as tools for
CC identifying agents active against ovarian cancer, or to prepare
CC medicaments for treating ovarian cancer. The cDNA sequences can be used
CC to obtain genomic genes, their promoters, enhancers, silencers, exon
CC structures, intron structures and their splice variants. AA241222-241324
CC represent cDNA sequences derived from normal human ovarian tissue and
CC which encode the protein fragments represented in AAY59724-Y59837.
XX
SQ Sequence 1905 BP; 466 A; 489 C; 534 G; 416 T; 0 other:

Query Match	47.38;	Score 783;	DB 20;	Length 1905;
Best Local Similarity	99.68;	Pred. No. 0;		
Matches	983;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0

QY	659	CAAGAAGGGAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCTATGCCCCG	718
Db	895	CAAGAAGCGAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCTATGCCCCG	954
QY	719	GACAGACCTGAGAAGAATCGGGACTACCCCACTAGCCCTCCAAGATGCCAAGAAACAGCT	778
Db	955	GACAGACCTGAGAAGAATCGGGACTACCCCACTAGCCCTCCAAGATGCCAAGAAACAGCT	1014
QY	779	GCTGTGTGGGGCAGCCATTTGGCACTCATGAGGATGACAAGTATAGGCTGGAAGCTTGCCTGC	838
Db	1015	GCTGTGTGGGGCAGCCATTTGGCACTCATGAGGATGACAAGTATAGGCTGGAAGCTTGCCTGC	1074
QY	839	CCAGGCTGTGTGATGTAGTGTGTTGGACTCTTCCAGGGAATTCATCTTCCAGAT	898
Db	1075	CCAGGCTGTGTGATGTAGTGTGTTGGACTCTTCCAGGGAATTCATCTTCCAGAT	1134
QY	899	CAATATGATCAAGTACATCAAAAGCAAAATACCCTAATCTCCAAGTCAATGGAGCAATGT	958
Db	1135	CAATATGATCAAGTACATCAAAAGCAAAATACCCTAATCTCCAAGTCAATGGAGCAATGT	1194
QY	959	GCTCACTGCTGCCAGGCCCAAGAACTCATTTGATGCAGGTGTGATGCGCTGCGGGTGGG	1018
Db	1195	GCTCACTGCTGCCAGGCCCAAGAACTCATTTGATGCAGGTGTGATGCGCTGCGGGTGGG	1254
QY	1019	CATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGCGGCCCCCAAGC	1078
Db	1255	CATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGCGGCCCCCAAGC	1314
QY	1079	AACAGCAGTGTACAAGGTGTATGATATGCACGCGCTTTGGTGTCCGGTCAATTGCTGA	1138
Db	1315	AACAGCAGTGTACAAGGTGTCAAGTATGCACGCGCTTTGGTGTCCGGTCAATTGCTGA	1374
QY	1139	TGGAGGAATCCAAATGTGGGTCAATATTGCGAAAGCCTTGGCCCTTGGGGCCTCCACAGT	1198
Db	1375	TGGAGGAATCCAAATGTGGGTCAATATTGCGAAAGCCTTGGCCCTTGGGGCCTCCACAGT	1434
QY	1199	CATGATGGGCTCTCTCCTGGCTGCCACCACCTGAGGCCCTGGTGAATACTTCTTTCCGA	1258
Db	1435	CATGATGGGCTCTCTCCTGGCTGCCACCACCTGAGGCCCTGGTGAATACTTCTTTCCGA	1494
QY	1259	TGGGATCCGGCTAAAGAAATATCGCGGTATGGGTCTCTCGATGCCATGGACAAGCACCT	1318
Db	1495	TGGGATCCGGCTAAAGAAATATCGCGGTATGGGTCTCTCGATGCCATGGACAAGCACCT	1554
QY	1319	CAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAAATCAAAGTGGCCCCAGGGAGTGT	1378
Db	1555	CAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAAATCAAAGTGGCCCCAGGGAGTGT	1614
QY	1379	TGCTGCTGTGCAGGACAAAGGCTCAATCCACAAATTTGTCCCTTACCTGATTTGCTGGCAT	1438
Db	1615	TGCTGCTGTGCAGGACAAAGGCTCAATCCACAAATTTGTCCCTTACCTGATTTGCTGGCAT	1674

QY 1439 CCAACACTCATGCCAGGACATTGGTCCCAAGCCTTGACCCAAAGTCCGAGCCATGATGTA 1498
| | | | |
Db 1675 CCAACACTCATGCCAGGACATTGGTCCCAAGCCTTGACCCAAAGTCCGAGCCATGATGTA 1734
QY 1499 CTCTGGGAGCTTAAGTTTGAGAGAGAACGCTCTCAGCCAGGTGGAAGGTGGCGTCCA 1558
| | | | |
Db 1735 CTCTGGGAGCTTAAGTTTGAGAGAGAACGCTCTCAGCCAGGTGGAAGGTGGCGTCCA 1794
QY 1559 TAGCCTCCATTCGTATGAGAAAGCGCTTTTCTGA AAAAGGATCCAGACACCTCCTCGGT 1618
| | | | |
Db 1795 TAGCCTCCATTCGTATGAGAAAGCGCTTTTCTGA AAAAGGATCCAGACACCTCCTCGGT 1854
QY 1619 TTTT TTTTCAATAAAGTTTAGAAGA 1645
| | | | |
Db 1855 TTTT TTTTCAATAAAGTTTAGAAGA 1881
RESULT 7
AAF21634
ID AAF21634 standard; DNA; 2019 BP.
XX
AC AAF21634;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 21.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antilucer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS Homo sapiens.
XX
PN WO200055173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05881.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-611515/58.
DR P-PsDB; AAB58731.
XX
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
XX
PS Claim 1: Page 496; 1299pp; English.
XX
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antiinflammatory; antilucer; vulnerary; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiant activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and agonists may also be used in the diagnosis,

CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemias; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.
XX
SQ Sequence 2019 BP; 512 A; 483 C; 538 G; 476 T; 10 other;
Query Match 40.0%; Score 662; DB 21; Length 2019;
Best Local Similarity 99.5%; Pred. No. 6.8e-306;
Matches 982; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 659 CAAGAAGGAAAGTTGCCCATTTGTAATGAGATGATGAGCTTTGGCCATCATTTGCCCG 718
| | | | |
Db 985 CAAGAAGGAAAGTTGCCCATTTGTAATGAGATGATGAGCTTTGGCCATCATTTGCCCG 1044
QY 719 GACAGACCTGAAGAAGATTCGGACTACCCACTAGCCTCCAAGATGCCAAGAACAGCT 778
| | | | |
Db 1045 GACAGACCTGAAGAAGATTCGGACTACCCACTAGCCTCCAAGATGCCAAGAACAGCT 1104
QY 779 GCTGTGTGGGCGCCATTTGGCACTCATGAGATGACAAAGTATAGGCTGCACTTGCTCCG 838
| | | | |
Db 1105 GCTGTGTGGGCGCCATTTGGCACTCATGAGATGACAAAGTATAGGCTGCACTTGCTCCG 1164
QY 839 CCAGGCTGGTGGATGTAGTGGTTTGGACTCTTCCAGGAAATTCATCTTCCAGAT 898
| | | | |
Db 1165 CCAGGCTGGTGGATGTAGTGGTTTGGACTCTTCCAGGAAATTCATCTTCCAGAT 1224
QY 899 CAATATGATCAAGTACATCAAGACAAATACCCTAATCTCCAAGTCAATGGAGGCAATGT 958
| | | | |
Db 1225 CAATATGATCAAGTACATCAAGACAAATACCCTAATCTCCAAGTCAATGGAGGCAATGT 1284
QY 959 GGTCACTGCTGCCCGCAGGCCAAGAACCCTCATTTGATGACGGTGTGATGCCCTGCGGTGGG 1018
| | | | |
Db 1285 GGTCACTGCTGCCCGCAGGCCAAGAACCCTCATTTGATGACGGTGTGATGCCCTGCGGTGGG 1344
QY 1019 CATGGAAAGTGGCTCCATCTGCAATTATCCAGAAAGTGCTGGCCTGTGGCGGCCCAAGC 1078
| | | | |
Db 1345 CATGGAAAGTGGCTCCATCTGCAATTATCCAGAAAGTGCTGGCCTGTGGCGGCCCAAGC 1404
QY 1079 AACAGCAGTGTACAAGGTGTATGAGTATGCACGGCGCTTTGGTGTCCGGTCAATTGCTGA 1138
| | | | |
Db 1405 AACAGCAGTGTACAAGGTGTCAAGAGTATGCACGGCGCTTTGGTGTCCGGTCAATTGCTGA 1464
QY 1139 TGGAGGAATCCAAATATGTGGTCAATATTTGGCAAAAGCCTTGCGCCCTCGCACAGT 1198
| | | | |
Db 1465 TGGAGGAATCCAAATATGTGGTCAATATTTGGCAAAAGCCTTGCGCCCTCGCACAGT 1523
QY 1199 CATGATGGGCTCTCTCTGCTGGCCACCACTGAGGCCCTGTGTAATCTCTTTTCCGA 1258
| | | | |
Db 1524 CATGATGGGCTCTCTCTGCTGGCCACCACTGAGGCCCTGTGTAATCTCTTTTCCGA 1583
QY 1259 TGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCACCT 1318
| | | | |
Db 1584 TGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCACCT 1643
QY 1319 CAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATCAAAAGTGGCCAGGAGTGTG 1378
| | | | |
Db 1644 CAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATCAAAAGTGGCCAGGAGTGTG 1703
QY 1379 TGGTGTGTGCAAGACAAGGGTCAATCCAAATTTTGTCCCTTACCTGATTTGCTGGCAT 1438
| | | | |
Db 1704 TGGTGTGTGCAAGACAAGGGTCAATCCAAATTTTGTCCCTTACCTGATTTGCTGGCAT 1763
QY 1439 CCAACACTCATGCCAGGACATTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTA 1498
| | | | |
Db 1764 CCAACACTCATGCCAGGACATTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTA 1823
QY 1499 CTCTGGGAGCTTAAGTTTGAGAGAGAACGCTCCTCAGCCAGGTGGAAGGTGGCGTCCA 1558
| | | | |
Db 1824 CTCTGGGAGCTTAAGTTTGAGAGAGAACGCTCCTCAGCCAGGTGGAAGGTGGCGTCCA 1883

QY	1559	TAGCCTCCATTCGTATGAGAACGCCGCTTTTCTGTGAAAGGATCCAGC	ACACCTCCTCGGT	1618
Db	1884	TAGCCTCCATTCGTATGAGAACGCCGCTTTTCTGTGAAAGGATCCAGC <td>ACACCTCCTCGGT</td> <td>1943</td>	ACACCTCCTCGGT	1943
QY	1619	TTTTTTTTCATATAAAGTTAGAAAGA	1645	
Db	1944	TTTTTTTTCATATAAAGTTAGAAAGA	1970	
RESULT 8				
AAD28929	ID	AAD28929 standard; DNA; 1158 BP.		
XX	AC	AAD28929;		
XX	DT	07-MAY-2002 (first entry)		
XX	DE	Human type II IMPDH-SPTQ variant DNA.		
XX	XX			
KW	KW	Human: inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;		
KW	KW	proliferative-type disease; cancer; imaging methodology; cytostatic;		
KW	KW	therapy: enzyme; variant; ds.		
XX	OS	Homo sapiens.		
OS	OS	Synthetic.		
XX	PN	WO200185952-A2.		
PD	XX	15-NOV-2001.		
XX	PF	10-MAY-2001; 2001WO-US15457.		
XX	PR	10-MAY-2000; 2000US-203448P.		
XX	PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
PI	PI	Krystek SR, Sheriff S, Wiltmer MR, Hollenbaugh DL, Yan N;		
PI	PI	Mouravieff JE, Einspahr HM, Kish K;		
XX	DR	WPI: 2002-164105/21.		
PT	PT	New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide		
PT	PT	having an oligo-peptide domain substituted for a subdomain of a		
PT	PT	wild-type IMPDH polypeptide, useful in drug discovery or for generating		
PT	PT	antibodies -		
XX	PS	Claim 54; Fig 12; 161pp; English.		
XX	CC	The invention relates to modified inosine 5'-monophosphate dehydrogenase		
CC	CC	(IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain		
CC	CC	substituted for a subdomain of a wild-type IMPDH polypeptide. The		
CC	CC	modified IMPDH polypeptides are useful for drug discovery, for		
CC	CC	therapeutic, diagnostic and prognostic procedures for detecting or		
CC	CC	quantifying modified IMPDH polypeptides and their corresponding nucleic		
CC	CC	acids. IMPDH polypeptides are also useful for generating antibodies, as		
CC	CC	diagnostic and prognostic markers of diseases, as targets for various		
CC	CC	therapeutic modalities, and to identify and isolate ligands and other		
CC	CC	agents that bind to modified IMPDH. These antibodies may be used in		
CC	CC	diagnostic assays, imaging methodologies, therapeutic methods in the		
CC	CC	management of cancer or other proliferative-type diseases, and in		
CC	CC	purifying modified IMPDH polypeptides and for isolating related		
CC	CC	molecules such as wild type and mutant IMPDH polypeptides. The present		
CC	CC	sequence is human type II IMPDH-SPTQ variant DNA.		
XX	SO	Sequence 1158 BP; 279 A; 301 C; 310 G; 268 T; 0 other;		
QY	774	CAGCTGCTGTGTGGGGCAGCCATTGGCACTCATGAGGATGACAAGTAAAGGCTGGACTTG	833	
Db	340	CAGCTGCTGTGTGGGGCAGCCATTGGCACTCATGAGGATGACAAGTAAAGGCTGGACTTG	399	
Query Match 37.2%; Score 615; DB 24; Length 1158;				
Best local Similarity 99.5%; Pred. No. 1.9e-283;				
Matches 815; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				

QY	834	CTCGCCACAGGCTGGTGTGGATGTAGTGGTTTGGACTCTTCCACAGGAAATTCATCTTC	893
Db	400	CTCGCCACAGGCTGGTGTGGATGTAGTGGTTTGGACTCTTCCACAGGAAATTCATCTTC	459
QY	894	CAGATCAATATGATCAAGTATACATCAAAAGCAAAATACCCTAATCTCAAGTCATTGAGGC	953
Db	460	CAGATCAATATGATCAAGTATACATCAAAAGCAAAATACCCTAATCTCAAGTCATTGAGGC	519
QY	954	AATGTGTCACCTGCTGCCAGGCCAAGACCTCATTTGATGCAGGTGTGGATGCCCTGGC	1011
Db	520	AATGTGTCACCTGCTGCCAGGCCAAGACCTCATTTGATGCAGGTGTGGATGCCCTGGC	579
QY	1014	GTGGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGCCTGTGGCGGCC	107
Db	580	GTGGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGCCTGTGGCGGCC	639
QY	1074	CAAGCAACAGCAGTGTACAAAGGTGTATGAGTATGCACGGCGCTTGGTCCGGTCATT	1133
Db	640	CAAGCAACAGCAGTGTACAAAGGTGTACAGTATGCACGGCGCTTGGTCCGGTCATT	699
QY	1134	GCTGATGGAGAAATCCAAATGTGGGTATATTTGCCAAAGCCTTGGCCCTTGCGCCTCC	119
Db	700	GCTGATGGAGAAATCCAAATGTGGGTATATTTGCCAAAGCCTTGGCCCTTGCGCCTCC	759
QY	1194	ACAGTCATGATGGGCTCTCTCCTGGCTGCCACCACCTGAGGCCCCGTGTAATACTTCTTT	125
Db	760	ACAGTCATGATGGGCTCTCTCCTGGCTGCCACCACCTGAGGCCCCGTGTAATACTTCTTT	819
QY	1254	TCCGATGGGATCCGGCTAAAGAAATATCGCCGTATGGGTCTCTTCGATGCCATGGACAC	131
Db	820	TCCGATGGGATCCGGCTAAAGAAATATCGCCGTATGGGTCTCTTCGATGCCATGGACAC	879
QY	1314	CACCTCAGCAAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATTCAAAGTGGCCAGGGA	137
Db	880	CACCTCAGCAAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATTCAAAGTGGCCAGGGA	939
QY	1374	GTGTCTGGTCTGTTCAGGACAAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCT	143
Db	940	GTGTCTGGTCTGTTCAGGACAAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCT	999
QY	1434	GGCATCCAACACTCATGCGCAGGACATTGGTGCCAAAGAGCTTGACCCCAAGTCCGAGCCATG	149
Db	1000	GGCATCCAACACTCATGCGCAGGACATTGGTGCCAAAGAGCTTGACCCCAAGTCCGAGCCATG	105
QY	1494	ATGTACTCTGGGGAGCTTAAGTTTGAGAGAAGAACGTCCCTCAGCCCAAGTGGGAAGTGGC	155
Db	1060	ATGTACTCTGGGGAGCTTAAGTTTGAGAGAAGAACGTCCCTCAGCCCAAGTGGGAAGTGGC	111
QY	1554	GTCCATAGCCCTCCATTCGTATGAGGAAGCGGCTTTCTGA	1592
Db	1120	GTCCATAGCCCTCCATTCGTATGAGGAAGCGGCTTTCTGA	1158
RESULT 9			
AAD28927			
ID	AAD28927	standard; cDNA; 1158 BP.	
XX	XX		
AC	AAD28927;		
XX	XX		
DT	07-MAY-2002	(first entry)	
XX	XX		
DE	Human type II IMPDH-AGRP variant cDNA.		
XX	XX		
KW	Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;		
KW	proliferative-type disease; cancer; imaging methodology; cytostatic;		
KW	therapy; enzyme; variant; ss.		
XX	XX		
OS	Homo sapiens.		
OS	Synthetic.		
XX	XX		
Key	Location/Qualifiers		
FT	CDS	1..1158	

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FT      /*tag= a
FT      /product= "Human type II IMPDH-AGRP variant"
XX
PN      WO200185952-A2.
XX
PD      15-NOV-2001.
XX
PF      10-MAY-2001; 2001WO-US15457.
XX
PR      10-MAY-2000; 2000US-203448P.
XX
PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI      Krystek SR, Sheriff S, Wilmer MR, Hollenbaugh DL, Yan N;
PI      Mouravieff JE, Einspahr HM, Kish K;
XX
DR      WPI; 2002-164105/21.
DR      P-PSDB; AAE18181.
XX
PT      New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT      having an oligo-peptide domain substituted for a subdomain of a
PT      wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT      antibodies -
XX
XX      Claim 54; Fig 14; 161pp; English.
XX
XX      The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC      (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC      substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC      modified IMPDH polypeptides are useful for drug discovery, for
CC      therapeutic, diagnostic and prognostic procedures for detecting or
CC      quantifying modified IMPDH polypeptides and their corresponding nucleic
CC      acids. IMPDH polypeptides are also useful for generating antibodies, as
CC      diagnostic and prognostic markers of diseases, as targets for various
CC      therapeutic modalities, and to identify and isolate ligands and other
CC      agents that bind to modified IMPDH. These antibodies may be used in
CC      diagnostic assays, imaging methodologies, therapeutic methods in the
CC      management of cancer or other proliferative-type diseases, and in
CC      purifying modified IMPDH polypeptides and for isolating related
CC      molecules such as wild type and mutant IMPDH polypeptides. The present
CC      sequence is human type II IMPDH-AGRP variant cDNA.
XX
SQ      Sequence 1158 BP; 277 A; 300 C; 313 G; 268 T; 0 other;
      Query Match      37.1%; Score 613; DB 24; Length 1158;
      Best Local Similarity 99.5%; Pred. No. 1.7e-282;
      Matches 813; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db      702 TGATGGAGGAATCCAAATGTGGGTCATATATGGCAAGCCTTGCCCTGGGCCCTCCAC 761
QY      1196 AGTCATGATGGGCTCTCTCCTGGCTGCCACCACATGAGGCCCTGGTGAATACTTCTTTC 1255
Db      762 AGTCATGATGGGCTCTCTCCTGGCTGCCACCACATGAGGCCCTGGTGAATACTTCTTTC 821
QY      1256 CGATGGGATCCGGCTTAAGAAATATATCGCGGTATGGGTTCTCTCGATGCCATGACAAGCA 1315
Db      822 CGATGGGATCCGGCTTAAGAAATATATCGCGGTATGGGTTCTCTCGATGCCATGACAAGCA 881
QY      1316 CCTCAGCAGCCAGAACAGATATTTCACTGAAGCTGACAAATCAAAGTGCCCGAGGAGT 1375
Db      882 CCTCAGCAGCCAGAACAGATATTTCACTGAAGCTGACAAATCAAAGTGCCCGAGGAGT 941
QY      1376 GTCGTGCTGTGTCAGAGCAAAAGGTCATCCACAAATTTGTCCTTACCTGATTCCTGG 1435
Db      942 GTCTGGTGTGTGTCAGAGCAAAAGGTCATCCACAAATTTGTCCTTACCTGATTCCTGG 1001
QY      1436 CATCCAACACTCATGCCAGGACATTTGGTGCCAAAGCTTGACCCCAAGTCCGAGCCATGAT 1495
Db      1002 CATCCAACACTCATGCCAGGACATTTGGTGCCAAAGCTTGACCCCAAGTCCGAGCCATGAT 1061
QY      1496 GTACTCTGGGAGCTTAAGTTTGAGAAGAGAAGCTTCACGCCAGGTGGAAGTGGCGT 1555
Db      1062 GTACTCTGGGAGCTTAAGTTTGAGAAGAGAAGCTTCACGCCAGGTGGAAGTGGCGT 1121
QY      1556 CCATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA 1592
Db      1122 CCATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA 1158

RESULT 10
AAD28922
ID      AAD28922 standard; cDNA; 1155 BP.
XX
AC      AAD28922;
XX
DT      07-MAY-2002 (first entry)
XX
DE      Human type II IMPDH-DKT variant cDNA.
XX
KW      Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW      proliferative-type disease; cancer; imaging methodology; cytostatic;
KW      therapy; enzyme; variant; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
FH      Key      Location/Qualifiers
FT      CDS      1..1155
FT      CDS      /*tag= a
FT      CDS      /product= "Human type II IMPDH-DKT variant"
XX
XX      WO200185952-A2.
XX
XX      15-NOV-2001.
XX
XX      10-MAY-2001; 2001WO-US15457.
XX
XX      10-MAY-2000; 2000US-203448P.
XX
XX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX      Krystek SR, Sheriff S, Wilmer MR, Hollenbaugh DL, Yan N;
XX      Mouravieff JE, Einspahr HM, Kish K;
XX
XX      WPI; 2002-164105/21.
XX      P-PSDB; AAE18181.
XX
XX      New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
XX      having an oligo-peptide domain substituted for a subdomain of a
XX      wild-type IMPDH polypeptide, useful in drug discovery or for generating
```


Query Match	37.0%;	Score 612;	DB 24;	Length 1155;	
Best Local Similarity	99.5%;	Pred. No. 5.2e-282;			
Matches 812;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;	
QY	777 CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGGCTC	836			
Db	340 CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGGCTC	399			
QY	837 GCCCAGGCTGGTGTGGATGTAGTGGTTTTGGACTCTTCCAGGGAATTCATCTTCCAG	896			
Db	400 GCCCAGGCTGGTGTGGATGTAGTGGTTTTGGACTCTTCCAGGGAATTCATCTTCCAG	459			
QY	897 ATCAATATGATCAAGTACATCAAGACAATACCCTAATCTCCAAGTCATTTGAGGCAAT	956			
Db	460 ATCAATATGATCAAGTACATCAAGACAATACCCTAATCTCCAAGTCATTTGAGGCAAT	519			
QY	957 GTGTCACCTGCTGCCAGGCGCAAGAACCTTCATTGATGCAGGTGTGGATGCCCTGGGGTG	1016			
Db	520 GTGTCACCTGCTGCCAGGCGCAAGAACCTTCATTGATGCAGGTGTGGATGCCCTGGGGTG	579			
QY	1017 GGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCCCTGTGGGGCGGCCAA	1076			
Db	580 GGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCCCTGTGGGGCGGCCAA	639			
QY	1077 GCAACAGCAGTGTACAAAGGTGTATGAGTATGCACGGCGCTTGTGTTCCGGTCATTGCT	1136			
Db	640 GCAACAGCAGTGTACAAAGGTGTACAGATATGCACGGCGCTTGTGTTCCGGTCATTGCT	699			
QY	1137 GATGAGGAATCCAAATGTGGGTTCATATTCGAAAGCCCTTGCCCTTGGGGCCTCCACA	1196			
Db	700 GATGAGGAATCCAAATGTGGGTTCATATTCGAAAGCCCTTGCCCTTGGGGCCTCCACA	759			
QY	1197 GTCATGATGGGCTCTCTCCTGGCTGCCACCACTGAGGCCCTGTGTAATACTTCTTTCC	1256			
Db	760 GTCATGATGGGCTCTCTCCTGGCTGCCACCACTGAGGCCCTGTGTAATACTTCTTTCC	819			
QY	1257 GATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTCTCTCGATGCCATGGACAAGCAC	1316			
Db	820 GATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTCTCTCGATGCCATGGACAAGCAC	879			
QY	1317 CTCAGCAGCCAGACAAGATATTTCAGTGAAGCTGCACAAATCAAAGTGGCCCCAGGGAGTG	1376			
Db	880 CTCAGCAGCCAGACAAGATATTTCAGTGAAGCTGCACAAATCAAAGTGGCCCCAGGGAGTG	939			
QY	1377 TCTGTGCTGTGCAGGACAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGC	1436			
Db	940 TCTGTGCTGTGCAGGACAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGC	999			
QY	1437 ATCCAACACTCATGCCAGGACATTTGTGCCAAGAGCTTGACCCAAAGTCCGAGCCATGATG	1496			
Db	1000 ATCCAACACTCATGCCAGGACATTTGTGCCAAGAGCTTGACCCAAAGTCCGAGCCATGATG	1059			
QY	1497 TACTCTGGGAGCTTAAGTTTGAGAAGAGAAGCTCCTCAGCCCAAGTGAAGGTGGCGTC	1556			
Db	1060 TACTCTGGGAGCTTAAGTTTGAGAAGAGAAGCTCCTCAGCCCAAGTGAAGGTGGCGTC	1119			
QY	1557 CATAGCCTCCATTTCGTATGAGAAGCGGCTTTCTGA	1592			
Db	1120 CATAGCCTCCATTTCGTATGAGAAGCGGCTTTCTGA	1155			
RESULT 12					
ID	AAD28924	standard; cDNA; 1155 BP.			
XX	AAD28924;				
AC	AAD28924;				
XX	07-MAY-2002	(first entry)			
DT	07-MAY-2002	(first entry)			
XX	Human type II IMPDH-SPT variant cDNA.				
DE	Human type II IMPDH-SPT variant cDNA.				
XX	Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;				
KW	proliferative-type disease; cancer; imaging methodology; cytostatic;				
KW	proliferative-type disease; cancer; imaging methodology; cytostatic;				

KW	therapy; enzyme; variant; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	key
FT	CDS
FT	location/Qualifiers
FT	1..1155
FT	/tag= a
FT	/product= "Human type II IMPDH-SPT variant"
PN	WO200185952-A2.
XX	
PD	15-NOV-2001.
XX	
PF	10-MAY-2001; 2001WO-US15457.
XX	
PR	10-MAY-2000; 2000US-203448P.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Krystek SR, Sherif S, Wilmer MR, Hollenbaugh DL, Yan N;
PI	Mouravieff JE, Einspahr HM, Kish K;
XX	
DR	WPI: 2002-164105/21.
DR	P-PSDB; AAEL8172.
XX	
PT	New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT	having an oligo-peptide domain substituted for a subdomain of a
PT	wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT	antibodies -
XX	
PS	Claim 54; Fig 11; 161pp; English.
XX	
CC	The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC	(IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC	substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC	modified IMPDH polypeptides are useful for drug discovery, for
CC	therapeutic, diagnostic and prognostic procedures for detecting or
CC	quantifying modified IMPDH polypeptides and their corresponding nucleic
CC	acids. IMPDH polypeptides are also useful for generating antibodies, as
CC	diagnostic and prognostic markers of diseases, as targets for various
CC	therapeutic modalities, and to identify and isolate ligands and other
CC	agents that bind to modified IMPDH. These antibodies may be used in
CC	diagnostic assays, imaging methodologies, therapeutic methods in the
CC	management of cancer or other proliferative-type diseases, and in
CC	purifying modified IMPDH polypeptides and for isolating related
CC	molecules such as wild type and mutant IMPDH polypeptides. The present
CC	sequence is human type II IMPDH-SPT variant cDNA.
XX	
SQ	Sequence 1155 BP; 278 A; 300 C; 309 G; 268 T; 0 other;
Query Match	
Best Local Similarity 37.0%;	
Score 612; DB 24; Length 1155;	
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	777 CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGGCTC 836
Db	340 CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGGCTC 399
QY	837 GCCCAGGCTGGTGTGGATGTAGTGGTTTTGGACTCTTCCAGGGAATTCATCTTCCAG 896
Db	400 GCCCAGGCTGGTGTGGATGTAGTGGTTTTGGACTCTTCCAGGGAATTCATCTTCCAG 459
QY	897 ATCAATATGATCAAGTACATCAAGACAATACCCTAATCTCCAAGTCATTGAGGCAAT 956
Db	460 ATCAATATGATCAAGTACATCAAGACAATACCCTAATCTCCAAGTCATTGAGGCAAT 519
QY	957 GTGTCACCTGCTGCCAGGCGCAAGAACCTCATTTGATGCAGGTGTGGATGCCCTGGGGTG 1016
Db	520 GTGTCACCTGCTGCCAGGCGCAAGAACCTCATTTGATGCAGGTGTGGATGCCCTGGGGTG 579
QY	1017 GGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCCCTGTGGGGCGGCCCAA 1076

Db	580	GGCATGGGAAGTGGCTCCATCTGCATTACGCAGGAAGTGC	GGGGCGGCCCCAA	639	
OY	1077	GCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCGCTTTGGTGT	CCGGTCAATTGCT	1136	
Db	640	GCAACAGCAGTGTACAAAGTGTACAGATATGCACGGCGCTTTGGTGT	CCGGTCAATTGCT	699	
OY	1137	GATGGAGGAATCCAAAATGTGGGTATATTTGCCAAAGCCTTGCCCT	GGGGCTCCACA	1196	
Db	700	GATGGAGGAATCCAAAATGTGGGTATATTTGCCAAAGCCTTGCCCT	GGGGCTCCACA	759	
OY	1197	GTCATGATGGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCTGGTGA	TACTTCTTTCC	1256	
Db	760	GTCATGATGGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCTGGTGA	TACTTCTTTCC	819	
OY	1257	GATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGC	ATGGACAAGCAC	1316	
Db	820	GATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGC	ATGGACAAGCAC	879	
OY	1317	CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAAATCAAAAGT	GCCCGAGGAGTG	1376	
Db	880	CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAAATCAAAAGT	GCCCGAGGAGTG	939	
OY	1377	TCTGCTGCTGTGCAGGACAAAGGTCATATCCACAATTTGTCCCTTA	CTGATTGCTGGC	1436	
Db	940	TCTGCTGCTGTGCAGGACAAAGGTCATATCCACAATTTGTCCCTTA	CTGATTGCTGGC	999	
OY	1437	ATCCAACACTCATGCCAGACATTTGGTGCCCAAGCCTTGACCCCAAGT	CGAGCCATGATG	1496	
Db	1000	ATCCAACACTCATGCCAGACATTTGGTGCCCAAGCCTTGACCCCAAGT	CGAGCCATGATG	1059	
OY	1497	TACTCTGGGAGCCTTAAGTTTGAGAAGAGAACGCTCTCAGCCAGGT	GAAGTGGCGTC	1556	
Db	1060	TACTCTGGGAGCCTTAAGTTTGAGAAGAGAACGCTCTCAGCCAGGT	GAAGTGGCGTC	1119	
OY	1557	CATAGCCTCCATTGCTATGAGAAGCGGCTTTCTGA	1592		
Db	1120	CATAGCCTCCATTGCTATGAGAAGCGGCTTTCTGA	1155		
RESULT 13					
AAD28925					
ID	AAD28925 standard; cDNA: 1155 BP.				
XX					
AC	AAD28925;				
XX					
DT	07-MAY-2002 (first entry)				
XX					
DE	Human type II IMPDH-GSG variant cDNA.				
XX					
KM	Human: inosine 5'-monophosphate dehydrogenase; IMPDH			drug discovery;	
KW	proliferative-type disease; cancer; imaging methodology; cytostatic;				
KW	therapy; enzyme; variant; ss.				
XX					
OS	Homo sapiens.				
OS	Synthetic.				
XX					
FH	Key			Location/Qualifiers	
FT	CDS				
FT	1.1155				
FT	/*tag= a			/product= "Human type II IMPDH-GSG variant"	
FT	/product=				
XX					
PN	W0200185952-A2.				
XX					
PD	15-NOV-2001.				
XX					
PF	10-MAY-2001; 2001WO-US15457.				
XX					
PR	10-MAY-2000; 2000US-203448P.				
XX					
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.				
XX					
PI	Krystek SR, Sherif S, Witmer MR, Hollenbaugh DL,			Yan N;	
PI	Mouravieff JE, Einspahr HM, Kish K;				

XX										
DR	WPI: 2002-164105/21.									
DR	P-PSDB: AAE18174.									
XX										
PT	New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide									
PT	having an oligo-peptide domain substituted for a subdomain of a									
PT	wild-type IMPDH polypeptide, useful in drug discovery or for generating									
PT	antibodies -									
XX										
PS	Claim 54; Fig 9; 161pp; English.									
XX										
CC	The invention relates to modified inosine 5'-monophosphate dehydrogenase									
CC	(IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain									
CC	substituted for a subdomain of a wild-type IMPDH polypeptide. The									
CC	modified IMPDH polypeptides are useful for drug discovery, for									
CC	therapeutic, diagnostic and prognostic procedures for detecting or									
CC	quantifying modified IMPDH polypeptides and their corresponding nucleic									
CC	acids. IMPDH polypeptides are also useful for generating antibodies, as									
CC	diagnostic and prognostic markers of diseases, as targets for various									
CC	therapeutic modalities, and to identify and isolate ligands and other									
CC	agents that bind to modified IMPDH. These antibodies may be used in									
CC	diagnostic assays, imaging methodologies, therapeutic methods in the									
CC	management of cancer or other proliferative-type diseases, and in									
CC	purifying modified IMPDH polypeptides and for isolating related									
CC	molecules such as wild type and mutant IMPDH polypeptides. The present									
CC	sequence is human type II IMPDH-GSG variant cDNA.									
XX										
SQ	Sequence 1155 BP; 277 A; 299 C; 312 G; 267 T; 0 other;									
Query Match 37.0%; Score 612; DB 24; Length 1155;										
Best Local Similarity 99.5%; Pred. No. 5.2e-282;										
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;										
OY	777	CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGCTC	836							
Db	340	CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGCTC	399							
OY	837	GCCCAGGCTGTGTGATGTAGTGTGTTGGACTCTTCCAGGGAATTCATCTTCCAG	896							
Db	400	GCCCAGGCTGTGTGATGTAGTGTGTTGGACTCTTCCAGGGAATTCATCTTCCAG	459							
OY	897	ATCAATATGATCAAGTACATCAAGACAATAATACCCTAATCTCCAAGTCAATTGGAGCAAT	956							
Db	460	ATCAATATGATCAAGTACATCAAGACAATAATACCCTAATCTCCAAGTCAATTGGAGCAAT	519							
OY	957	GTGTCACCTGCTGCCAGGCCAAGACCTCATTTGATGCAGGTGTGATGCCCTGCGGGTG	1016							
Db	520	GTGTCACCTGCTGCCAGGCCAAGACCTCATTTGATGCAGGTGTGATGCCCTGCGGGTG	579							
OY	1017	GGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGTGGCTGTGGCGGGCCCCAA	1076							
Db	580	GGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGTGGCTGTGGCGGGCCCCAA	639							
OY	1077	GCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCGCTTTGGTTCGGTCAATTGCT	1136							
Db	640	GCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCGCTTTGGTTCGGTCAATTGCT	699							
OY	1137	GATGGAGGAATCCAAAATGTGGGTATATTCGAAAGCCTTGCGCCCTTGCGGCTCCACA	1196							
Db	700	GATGGAGGAATCCAAAATGTGGGTATATTCGAAAGCCTTGCGCCCTTGCGGCTCCACA	759							
OY	1197	GTCATGATGGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCTGGTAATACTTCTTTCC	1256							
Db	760	GTCATGATGGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCTGGTAATACTTCTTTCC	819							
OY	1257	GATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGGAACAAGCAC	1316							
Db	820	GATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGGAACAAGCAC	879							
OY	1317	CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAAATCAAAAGTGGCCAGGAGTG	1376							
Db	880	CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAAATCAAAAGTGGCCAGGAGTG	939							

QY 1377 TCTGGTGTGTGCAGACAAAGGTCATCCACAATTTGTCCCTTACCTGATTCGTGGC 1436
CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CC 940 TCTGGTGTGTGCAGACAAAGGTCATCCACAATTTGTCCCTTACCTGATTCGTGGC 999
QY 1437 ATCCAACACTCATGCCAGACATTTGGTGCACAGACTTGACCCAACTGCCAGCATGATG 1496
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1000 ATCCAACACTCATGCCAGACATTTGGTGCACAGACTTGACCCAACTGCCAGCATGATG 1059
QY 1497 TACTCTGGGAGCTTAACTTTGAGAAGAACGTCCTCAGCCAGGTGGAAGTGGCGTC 1556
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1060 TACTCTGGGAGCTTAACTTTGAGAAGAACGTCCTCAGCCAGGTGGAAGTGGCGTC 1119
QY 1557 CATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA 1592
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1120 CATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA 1155
RESULT 14
AAD28928
ID AAD28928 standard; cDNA; 1158 BP.
XX
AC AAD28928;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human type II IMPDH-NSPL variant cDNA.
XX
KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW therapy; enzyme; variant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1158
FT /*tag= a
FT /product= "Human type II IMPDH-NSPL variant"
XX
PN WO200185952-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US15457.
XX
PR 10-MAY-2000; 2000US-203448P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Krystek SR, Sheriff S, Wiltmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;
XX
DR WPI; 2002-164105/21.
DR P-PSDB; AAE18183.
XX
PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies
XX
PS Claim 54; Fig 16; 161pp; English.
XX
CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or
CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other
CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the

CC management of cancer or other proliferative-type diseases, and in
CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is human type II IMPDH-NSPL variant cDNA.
XX
SQ Sequence 1158 BP; 279 A; 301 C; 309 G; 269 T; 0 other;
Query Match 37.0%; Score 612; DB 24; Length 1158;
Best Local Similarity 99.5%; Pred. No. 5.2e-282;
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 777 CTGCTGTGGGGGACGCCATTGGCACTCATGAGGATGACAAATATAGGCTGGACTTGGCTC 836
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 343 CTGCTGTGGGGGACGCCATTGGCACTCATGAGGATGACAAATATAGGCTGGACTTGGCTC 402
QY 837 GCCCAGGCTGGTGTGATGTAGTGGTTTGGACTCTCCAGGGAATTCATCTTCCAG 896
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403 GCCCAGGCTGGTGTGATGTAGTGGTTTGGACTCTTCCAGGGAATTCATCTTCCAG 462
QY 897 ATCAATATGATCAAGTACATCAAAAGACAAATACCTAATCTCCAAGTCATTTGAGGCAAT 956
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 463 ATCAATATGATCAAGTACATCAAAAGACAAATACCTAATCTCCAAGTCATTTGAGGCAAT 522
QY 957 GTGTCACCTGCTGCCACGCCCAAGAACCTCATTTGACAGGTGTGATGCCCTGCGGGTG 1016
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 523 GTGTCACCTGCTGCCACGCCCAAGAACCTCATTTGACAGGTGTGATGCCCTGCGGGTG 582
QY 1017 GGCAATGGGAAGTGGCTCCATCTGCATATATCCAGGAAGTGTGGCTGTGGCGGCCCCAA 1076
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 583 GGCAATGGGAAGTGGCTCCATCTGCATATATCCAGGAAGTGTGGCTGTGGCGGCCCCAA 642
QY 1077 GCAACAGCAGTGTACAAGGTGTATGATATGCAGCGGCGCTTGGTGTCCGGTCATTGCT 1136
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 643 GCAACAGCAGTGTACAAGGTGTCAAGTATGCACGCGCGCTTGGTGTCCGGTCATTGCT 702
QY 1137 GATGAGGAATCCAAATATGGGTCAATATGGCAAAAGCCTTGGCCCTTGGGCGCTCCACA 1196
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 703 GATGAGGAATCCAAATATGGGTCAATATGGCAAAAGCCTTGGCCCTTGGGCGCTCCACA 762
QY 1197 GTCATGATGGGCTCTCTCTGGCTGCCACCACTGAGGCCCTGGTGAATCTCTTTTCC 1256
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 763 GTCATGATGGGCTCTCTCTGGCTGCCACCACTGAGGCCCTGGTGAATCTCTTTTCC 822
QY 1257 GATGGGATCCGGCTAAAGAATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCAC 1316
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 823 GATGGGATCCGGCTAAAGAATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCAC 882
QY 1317 CTCAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATCAAAAGTGGCCCAAGGAGTG 1376
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 883 CTCAGCAGCCAGAACAGATATTTCAAGTGAAGCTGACAAATCAAAAGTGGCCCAAGGAGTG 942
QY 1377 TCTGGTGTGTGCAGGACAAAGGTCATCCACAATTTGTCCCTTACCTGATTCGTGGC 1436
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 943 TCTGGTGTGTGCAGGACAAAGGTCATCCACAATTTGTCCCTTACCTGATTCGTGGC 1002
QY 1437 ATCCAACACTCATGCCAGACATTTGGTGCACAGACTTGACCCAACTGCCAGCATGATG 1496
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1003 ATCCAACACTCATGCCAGACATTTGGTGCACAGACTTGACCCAACTGCCAGCATGATG 1062
QY 1497 TACTCTGGGAGCTTAACTTTGAGAAGAACGTCCTCAGCCAGGTGGAAGTGGCGTC 1556
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1063 TACTCTGGGAGCTTAACTTTGAGAAGAACGTCCTCAGCCAGGTGGAAGTGGCGTC 1122
QY 1557 CATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA 1592
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1123 CATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA 1158
RESULT 15
AAF18367
ID AAF18367 standard; DNA; 674 BP.
XX
AC AAF18367;

[illegible]

Db	182	CCTGAATTCACAGCCCAATGAGTTTCGAAAGTGAAGAAATATGAACAGGATTTCATCACA	241
QY	396	GACCTGTGTCCTCAGCCCCAAGATCGCGTGCGGATGTTTTGAGGCCAAGGCCCGG	455
Db	242	GACCTGTGTCCTCAGCCCCAAGATCGCGTGCGGATGTTTTGAGGCCAAGGCCCGG	301
QY	456	CATGTTCTGCGGTATCCCAATCAGACACAGGCCGGAATGGGAGCCGCTTGGTGGC	515
Db	302	CATGTTCTGCGGTATCCCAATCAGACACAGGCCGGAATGGGAGCCGCTTGGTGGC	361
QY	516	ATCATTCTCTCCAGGACATTGATTTTCTCAAGAGAGAGAACATGACTG	565
Db	362	ATCATTCTCTCCAGGACATTGATTTTCTCAAGAGAGAGAACATGACTG	411
RESULT 16			
ID	ABV44742	standard; cDNA; 607 BP.	
AC	ABV44742;		
DT	16-SEP-2002	(first entry)	
DE	Human prostate expression marker cDNA 44733.		
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;		
OS	Homo sapiens.		
PN	WO200160860-A2.		
PD	23-AUG-2001.		
PE	20-FEB-2001; 2001WO-US05171.		
XX	17-FEB-2000; 2000US-183319P.		
PR	16-MAR-2000; 2000US-189862P.		
PR	25-MAY-2000; 2000US-207454P.		
PR	09-JUN-2000; 2000US-211314P.		
PR	18-JUL-2000; 2000US-219007P.		
PR	13-DEC-2000; 2000US-255281P.		
PA	(MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.		
PI	Schlegel R, Endege WO, Monahan JE;		
DR	WPI; 2001-662795/76.		
XX	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -		
PS	Claim 1; Page 8871; 11750pp; English.		
XX	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:		
CC	(a) assessing whether a patient is afflicted with prostate cancer;		
CC	(b) monitoring the progression of prostate cancer in a patient;		
CC	(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;		
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;		
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;		
CC	(f) assessing the prostate cell carcinogenic potential of a compound;		
CC	(g) determining whether prostate cancer has metastasized in a patient;		
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a patient;		
CC	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.		
XX	Sequence 607BP: 141 A; 157 C; 171 G; 137 T; 1 other:		

Query Match		24.4%;	Score 404;	DB 23;	Length 607;
Best Local Similarity		100.0%;	Pred. No. 1.2e-182;		
Matches 404;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1101	GAGTATGCACGGCGCTTGGTGTCTCCGGTCATGTGCTGATGGAGAAATCCAAATGTGGGT	1160		
Db	194	GAGTATGCACGGCGCTTGGTGTCTCCGGTCATGTGCTGATGGAGAAATCCAAATGTGGGT	253		
QY	1161	CATATTGCCGAAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTGGCT	1220		
Db	254	CATATTGCCGAAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTGGCT	313		
QY	1221	GCCACCACTGAGGCCCCCTGGTGAATACTTCTTTCCGATGGATCCGGCTAAAGAAATAT	1280		
Db	314	GCCACCACTGAGGCCCCCTGGTGAATACTTCTTTCCGATGGATCCGGCTAAAGAAATAT	373		
QY	1281	CGCGGTATGGGTTCTCTCGATGCCATGACAAAGCACCTCAGCAGCCAGACAGATATTTTC	1340		
Db	374	CGCGGTATGGGTTCTCTCGATGCCATGACAAAGCACCTCAGCAGCCAGACAGATATTTTC	433		
QY	1341	AGTGAAGCTGACAAATCAAAAGTGGCCAGGGAGTGTCTGGTGTGAGAGACAAAGG	1400		
Db	434	AGTGAAGCTGACAAATCAAAAGTGGCCAGGGAGTGTCTGGTGTGAGAGACAAAGG	493		
QY	1401	TCAATCCACAAATTTGTCCCTTACCTGATTCCTGGCATCCAACACTCATGCCAGGACATT	1460		
Db	494	TCAATCCACAAATTTGTCCCTTACCTGATTCCTGGCATCCAACACTCATGCCAGGACATT	553		
QY	1461	GGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGG	1504		
Db	554	GGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGG	597		
RESULT 17					
ID	AAF94973				
AF	AAF94973 standard; cDNA; 396 BP.				
XX					
AC	AAF94973;				
XX					
DT	23-MAY-2001 (first entry)				
XX					
DE	Human ovarian cancer associated coding sequence SEQ ID NO: 164.				
XX					
KW	Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200118046-A2.				
XX					
PD	15-MAR-2001.				
XX					
PF	08-SEP-2000; 2000WO-US24827.				
XX					
PR	10-SEP-1999; 99US-0394374.				
PR	01-MAY-2000; 2000US-0561778.				
PR	15-AUG-2000; 2000US-0640173.				
PR	07-SEP-2000; 2000US-0656668.				
XX					
PA	(CORI-) CORIXA CORP.				
XX					
PI	Xu J, Stolk JA;				
XX					
DR	WPI; 2001-211395/21.				
XX					
PT	Isolated polypeptides associated with ovarian carcinomas, and the				
PT	nucleic acids that encode them, useful for the prevention diagnosis and				
PT	treatment of ovarian cancers -				
XX					
PS	Claim 18; Page 169; 189pp; English.				
XX					
CC	The present invention provides a number of coding sequences and proteins,				
CC	the over-expression of which is associated with ovarian carcinoma/cancer.				

CC	These can be used in the diagnosis, treatment and prevention of ovarian
CC	cancer, optionally by gene therapy or in the form of a vaccine. The
CC	present sequence is an example of one of these sequences.
XX	
SO	Sequence 396 BP; 96 A; 119 C; 96 G; 85 T; 0 other;
	Query Match 23.9%; Score 396; DB 22; Length 396;
	Best Local Similarity 100.0%; Pred. No. 8e-179;
	Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	21 GACACGGCGGCTGTCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGGCAGCTCC 80
Db	1 GACACGGCGGCTGTCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGGCAGCTCC 60
QY	81 TACGTGCCAGACGACGGACTCACAGCACAGCAGCTTCAACTGCCGAGACGGCTCACC 140
Db	61 TACGTGCCAGACGACGGACTCACAGCACAGCAGCTTCAACTGCCGAGACGGCTCACC 120
QY	141 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACCAGGTGACCTG 200
Db	121 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACCAGGTGACCTG 180
QY	201 ACTTCTGCTGTGACCAAGAAATCAGCTTTAAGACCCCACTGTTTCTCTCCCATGAC 260
Db	181 ACTTCTGCTGTGACCAAGAAATCAGCTTTAAGACCCCACTGTTTCTCTCCCATGAC 240
QY	261 ACAGTCACAGAGCTGGGATGGCCATAGCAATGGCGCTTACAGGCGGTATTGGCTTCATC 320
Db	241 ACAGTCACAGAGCTGGGATGGCCATAGCAATGGCGCTTACAGGCGGTATTGGCTTCATC 300
QY	321 CACCACAACGTGTACACCTGAATTCAGGCCAATGAAGTTCGGAAGTGAAGAAATATGAA 380
Db	301 CACCACAACGTGTACACCTGAATTCAGGCCAATGAAGTTCGGAAGTGAAGAAATATGAA 360
QY	381 CAGGATTCATCACAGACCCCTGTGGTCTCAGCCCC 416
Db	361 CAGGATTCATCACAGACCCCTGTGGTCTCAGCCCC 396
	RESULT 18
	ABT03240
ID	ABT03240 standard; cDNA; 396 BP.
XX	
AC	ABT03240;
XX	
DT	05-SEP-2002 (first entry)
XX	
DE	Human ovarian carcinoma associated coding sequence SEQ ID NO: 164.
XX	
KW	Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
KW	cytostatic; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200239885-A2.
XX	
PD	23-MAY-2002.
XX	
PF	13-NOV-2001; 2001WO-US45395.
XX	
PR	14-NOV-2000; 2000US-0713550.
PR	03-APR-2001; 2001US-0825294.
PR	02-OCT-2001; 2001US-0970966.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Stolk JA, Algate PA, Fling SP, Molesh DA;
XX	
DR	WPI; 2002-500186/53.
XX	
PT	Novel ovarian cancer polypeptide and polynucleotide, useful for
PT	detecting the presence of ovarian cancer in a patient, and in
PT	pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer

PT -
XX
PS Example 1; Page 169; 197pp; English.
XX
CC The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention.
XX
SQ Sequence 396 BP; 96 A; 119 C; 96 G; 85 T; 0 other;

Query Match 23.9%; Score 396; DB 24; Length 396;
Best Local Similarity 100.0%; Pred. No. 8e-179;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GACACGGCGGGTGTCTGTGTGGCCATGCCGACTACCTGATTAGTGGGGCAGCTCC 80
DB 1 GACACGGCGGGTGTCTGTGTGGCCATGCCGACTACCTGATTAGTGGGGCAGCTCC 60
QY 81 TACGTGCCAGACGACGACTCACAGCAGCAGCTCTTCAACTGCGGAGACGGCCTCACC 140
DB 61 TACGTGCCAGACGACGACTCACAGCAGCAGCTCTTCAACTGCGGAGACGGCCTCACC 120
QY 141 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACGAGTGACCTG 200
DB 121 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACGAGTGACCTG 180
QY 201 ACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCATGAC 260
DB 181 ACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCATGAC 240
QY 261 ACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGCTTACAGCGGCTATTGGCTTCATC 320
DB 241 ACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGCTTACAGCGGCTATTGGCTTCATC 300
QY 321 CACCACACTGTACACCTGAATTCAGGCCCAATGAAGTTCGGAAGTGAAGAATATGAA 380
DB 301 CACCACACTGTACACCTGAATTCAGGCCCAATGAAGTTCGGAAGTGAAGAATATGAA 360
QY 381 CAGGATTTCATCACAGACCCCTGTGTCTCAGCCCC 416
DB 361 CAGGATTTCATCACAGACCCCTGTGTCTCAGCCCC 396

RESULT 19
ABL48923
ID ABL48923 standard; cDNA; 396 BP.
XX
AC ABL48923;
XX
DT 18-JUN-2002 (first entry)
XX
DE Ovarian carcinoma sequence isolate 25775.
XX
KW Ovarian cancer; cancer therapy; vaccine; gene therapy
XX
OS Homo sapiens.
XX
PN US2002004491-A1.
XX
PD 10-JAN-2002.
XX
PF 03-APR-2001; 2001US-0825294.
XX
PR 10-SEP-1999; 99US-0394374.
PR 01-MAY-2000; 2000US-0561778.
PR 15-AUG-2000; 2000US-0640173.
PR 07-SEP-2000; 2000US-0656668.
PR 14-NOV-2000; 2000US-0713550.
XX
PA (XUJJ/) XU J.
PA (STOL/) STOLK J A.

PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
XX
PI Xu J, Stolk JA, Algate PA, Fling SP;
XX
DR WPI; 2002-171027/22.
XX

PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
PT prevention and/or treatment of cancer, especially ovarian cancer
XX
PS Example 1; Page 93; 131pp; English.

CC The invention relates to ovarian tumour polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or
CC gene therapy. Polypeptides and polynucleotides of the invention are
CC useful for detecting a cancer in a patient, for stimulating and/or
CC expanding T-cells specific for a tumour protein, and for inhibiting the
CC development of a cancer in a patient. They are also useful for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient and for determining the presence of a cancer in a patient.
CC The isolated polynucleotides of the invention are useful for their
CC ability to selectively form duplex molecules with complementary stretches
CC of the entire desired gene or gene fragments, and for designing and
CC preparing ribozyme molecules for inhibiting expression of tumour
CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
CC invention are also useful in recombinant DNA molecules to direct
CC expression of a polypeptide in appropriate host cells. The sequences
CC given in records ABL48760-ABL48956 represent polynucleotides encoding
XX ovarian carcinoma proteins.

SQ Sequence 396 BP; 96 A; 119 C; 96 G; 85 T; 0 other;

Query Match 23.9%; Score 396; DB 24; Length 396;
Best Local Similarity 100.0%; Pred. No. 8e-179;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GACACGGCGGGTGTCTGTGTGGCCATGCCGACTACCTGATTAGTGGGGCAGCTCC 80
DB 1 GACACGGCGGGTGTCTGTGTGGCCATGCCGACTACCTGATTAGTGGGGCAGCTCC 60
QY 81 TACGTGCCAGACGAGGACTCACAGCAGCAGCTCTTCAACTGGGAGACGGCCTCACC 140
DB 61 TACGTGCCAGACGAGGACTCACAGCAGCAGCTCTTCAACTGGGAGACGGCCTCACC 120
QY 141 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACGAGTGACCTG 200
DB 121 TACAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGACGAGTGACCTG 180
QY 201 ACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCATGAC 260
DB 181 ACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCCATGAC 240
QY 261 ACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGCTTACAGCGGCTATTGGCTTCATC 320
DB 241 ACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGCTTACAGCGGCTATTGGCTTCATC 300
QY 321 CACCACACTGTACACCTGAATTCAGGCCCAATGAAGTTCGGAAGTGAAGAATATGAA 380
DB 301 CACCACACTGTACACCTGAATTCAGGCCCAATGAAGTTCGGAAGTGAAGAATATGAA 360
QY 381 CAGGATTTCATCACAGACCCCTGTGTCTCAGCCCC 416
DB 361 CAGGATTTCATCACAGACCCCTGTGTCTCAGCCCC 396

RESULT 20
AAC03976
ID AAC03976 standard; cDNA; 554 BP.
XX
AC AAC03976;
XX
DT 06-OCT-2000 (first entry)
XX

DE Human secreted protein 5' EST, SEQ ID NO: 3974.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KM gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX EPI033401-A2.
PN
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
PX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
DR P-PsDB; AAG03970.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 3974; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors.
SQ Sequence 554 BP; 122 A; 159 C; 147 G; 118 T; 8 other;

Query Match	21.8%;	Score 361;	DB 21;	Length 554;
Best Local Similarity	100.0%;	Pred. No. 4.2e-162;		
Matches 361; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	9	GCGGTCTCTGGAGACACACGCGCGGTGTCTGTGTGGCCATGGCCGACTACCTGAATTAGT	68
Dd	25	GCGGTCTCTGGAGACACACGCGCGGTGTCTGTGTGGCCATGGCCGACTACCTGAATTAGT	84
OY	69	GGGGGCACGTCCTACGTGCCAGACGCGGACTCACAGCACAAGCTCTTCAACTGGCGA	128
Dd	85	GGGGGCACGTCCTACGTGCCAGACGCGGACTCACAGCACAAGCTCTTCAACTGGCGA	144
OY	129	GACGGCCTCACCTTACATGACTTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGAC	188
Dd	145	GACGGCCTCACCTTACATGACTTTTCTCATTTCTCCCTGGGTACATCGACTTCACCTGCAGAC	204
OY	189	CAGGTGACCTGACTTCTGCTGTGACCAAGAAATACACTTTTAAGACCACCACCTGGTTTTCC	248
Dd	205	CAGGTGACCTGACTTCTGCTGTGACCAAGAAATACACTTTTAAGACCACCACCTGGTTTTCC	264
OY	249	TCTCCCATGGACACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGTTACAGCGCGT	308
Dd	265	TCTCCCATGGACACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGTTACAGCGCGT	324
OY	309	ATTGGCTTCATCCACCACAACCTGTACACCTGAATTCCAGGCCAATGAAGTTCGGAAGTG	368
Dd	325	ATTGGCTTCATCCACCACAACCTGTACACCTGAATTCCAGGCCAATGAAGTTCGGAAGTG	384

QY	369	A	369
		1	
Db	385	A	385

RESULT	21
ABV37312/C	
ID	ABV37312 standard; cDNA; 420 BP.
XX	
AC	ABV37312;
XX	
DT	16-SEP-2002 (first entry)

DE Human prostate expression marker CDNA 37303.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN W0200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 25-MAY-2000; 2000US-207454P.

PR 18-JUL-2000; 2000US-219007P.
DD 13 DEC 2000 2000US 255301P

[illegible]

	TE.
	3
	b3
	McC
	EC
	c3
	E3
P	[c3]
cch]	[c3]
XX	
DT	

XX WBT : 2001-663705/76
DP

[illegible]

PT prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer stage of prostate cancer.

XX
DC
claim 1: Dano 7666, 1175000; Equal:ab

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

CC a nucleotide sequence given in Tables 1-9 (ABV000100-
CC specification or its complement (T) is useful for

CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient:

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

(f) assessing the prostate cell carcinogenic potential of a compound;

(h) assessing the appropriateness or indolence of prostate cancer in a

CC (I) is also useful as a pharmacodynamic marker

Sequence 420 BP: 87 A: 120 C: 105 G: 108 T: 0 other:
XX

```

Query Match      17.98;  Score 296;  DB 23;  Length 420;
Best Local Similarity 100.08;  Pred. No. 4.7e-131;
Matches 296;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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[illegible]

```
Db      338 TTGTAATGAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGAC TGAGAAGAATC 279
QY      739 GGGACTACCCACTAGCCTCCAAAGATGCCAAGACAGCTGCTGTGT GGGCAGCCATTG 798
      |||
Db      278 GGGACTACCCACTAGCCTCCAAAGATGCCAAGACAGCTGCTGTGT GGGCAGCCATTG 219
QY      799 GCACATCATGAGGATGACAAAGTATAGGCTGGACTTCTCGCCAGGCT GTGTGGATGTAG 858
      |||
Db      218 GCACATCATGAGGATGACAAAGTATAGGCTGGACTTCTCGCCAGGCT GTGTGGATGTAG 159
QY      859 TGGTTTGGACTCTTCCAGGGAATTCCATCTTCCAGATCAATATG TCAGACTAC 914
      |||
Db      158 TGGTTTGGACTCTTCCAGGGAATTCCATCTTCCAGATCAATATG TCAGACTAC 103
```

RESULT 22
AAZ80760
ID AAZ80760 standard; cDNA: 675 BP.

AC AAZ80760;

DT 07-APR-2000 (first entry)

DE Human colon cancer cell line SW480 cDNA clone SEQ ID NO:844.

KW Human; gene expression product; diagnosis; tumour; colon cancer;
KW colorectal adenocarcinoma; cell line SW480; cell proliferation;
KW cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
KW hyperplasia; ds.

OS Homo sapiens.

PN WO9964576-A2.

PD 16-DEC-1999.

PF 09-JUN-1999; 99WO-IB01062.

PR 10-JUN-1998; 98US-0088801.

PA (FARB) BAYER CORP.

PI Endege WO, Steinmann KE, Astle JH, Burgess CC, Bushnell SE;
PI Carroll E, Catino TJ, Derti A, Ford DM, Lewis ME, Monahan JE;
PI Schlegel R;

DR WPI; 2000-087220/07.

PT Novel nucleic acids, used to develop products for the diagnosis and
PT treatment of disorders involving unwanted cell proliferation,
PT particularly cancers, especially colon cancer -

PS Claim 15; Page 466-467; 469pp; English.

CC AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from
CC the human colorectal adenocarcinoma (colon cancer) cell line SW480. The
CC cDNA clones can be used to generate antisense oligonucleotides which
CC can be used for antisense therapy. Methods and products from the present
CC invention can be used for identifying and/or classifying cancerous cells
CC present in a human tumour, particularly in solid tumors, e.g.
CC carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones
CC can be used for developing agents for the diagnosis and treatment of
CC disorders involving unwanted cell proliferation, such as neoplasia,
CC dysplasia or hyperplasia.

CC Sequence 675 BP: 169 A; 150 C; 186 G; 161 T; 9 other;

CC Query Match 17.1%; Score 283; DB 21; Length 675;

CC Best Local Similarity 100.0%; Pred. No. 7.6e-125;

CC Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 GTACACCTGAATTCCAGGCCAATGAAGTTCGGAAGTGAAGAAATATGACAGGGATTCA 390
|||

```
Db      2 GTACACCTGAATTCCAGGCCCAATGAAGTTCGGAAGTGAAGAAATATGACAGGGATTCA 61
QY      391 TCACAGACCCGTGTGCTCTCAGCCCCCAAGATCGCGTGGATGTTTTGGAGCCCAAG 450
      |||
Db      62 TCACAGACCCGTGTGCTCTCAGCCCCCAAGATCGCGTGGATGTTTTGGAGCCCAAG 121
QY      451 CCGGCATGTTTCTCGGGTATCCCAATCACAGACAGCGCCGATGGGAGCCCGTTGG 510
      |||
Db      122 CCGGCATGTTTCTGCGGTATCCCAATCACAGACAGCGCCGATGGGAGCCCGTTGG 181
QY      511 TGGGCATCATCTCTCCAGGACATTTGATTTTCTCAAAAGAGAGGAACATGACTGTTCT 570
      |||
Db      182 TGGGCATCATCTCTCCAGGACATTTGATTTTCTCAAAAGAGAGGAACATGACTGTTCT 241
QY      571 TGAAGAGATTAATGACAAAGAGGGAAGACTTGTGTAGCCCC 613
      |||
Db      242 TGAAGAGATTAATGACAAAGAGGGAAGACTTGTGTAGCCCC 284
```

RESULT 23
ABV07378/c
ID ABV07378 standard; cDNA: 391 BP.

AC ABV07378;

DT 13-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 7369.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN WO200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

DR WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -

PS Claim 1; Page 1192; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;


```
PT Liver tissue sample
XX
PS Claim 1; SEQ ID NO 2197; 298bp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma, or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93003-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 6193 BP; 1404 A; 1597 C; 1628 G; 1564 T; 0 other;

Query Match          14.6%; Score 242; DB 24; Length 6193;
Best Local Similarity 100.0%; Pred. No. 2.8e-105;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1101 GAGTATGCACGGCGCTTGTGTTCCGGTCATGTGCTGATGAGAGAAATCAAATGTGGGT 1160
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 5210 GAGTATGCACGGCGCTTGTGTTCCGGTCATGTGCTGATGAGAGAAATCAAATGTGGGT 5269

QY 1161 CATATTGCGAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCTGGCT 1220
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 5270 CATATTGCGAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCTGGCT 5329

QY 1221 GCCACCACTGAGCCCCCTGTGTAATCTTTTTCGATGGGATCCGCTTAAAGAAATAT 1280
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 5330 GCCACCACTGAGCCCCCTGTGTAATCTTTTTCGATGGGATCCGCTTAAAGAAATAT 5389

QY 1281 CGCGTATGGTCTCTCGATGCCATGACACAGCAGCTCAGACGCCAGACAGATATTTC 1340
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 5390 CGCGTATGGTCTCTCGATGCCATGACACAGCAGCTCAGACGCCAGACAGATATTTC 5449

QY 1341 AG 1342
    ||
DB 5450 AG 5451

RESULT 26
ABQ58310
ID ABQ58310 standard; cDNA; 558 BP.
XX
AC ABQ58310;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:2005.
XX
KW Human; colon cancer; cancer; tissue profiling; forensics; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PE 02-OCT-2001; 2001WO-US30732.
XX
PR 02-OCT-2000; 2000US-237271P.
XX
PA (FARB ) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
```

```
PT Thiaglingam A, Lewis ME;
XX
PS WPI; 2002-426115/45.
XX
DR
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell
PT or tissue type, and in antisense therapy
XX
PS Claim 1; Fig 1; 796pp; English.
XX
ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists.
XX
SQ Sequence 558 BP; 151 A; 119 C; 143 G; 123 T; 22 other;

Query Match          13.9%; Score 230; DB 24; Length 558;
Best Local Similarity 100.0%; Pred. No. 1.6e-99;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TCCAGGCCAATGAAGTTCGAAAGTGAAGAAATATGACACAGGATTCATCACAGACCCTG 402
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 11 TCCAGGCCAATGAAGTTCGAAAGTGAAGAAATATGACACAGGATTCATCACAGACCCTG 70

QY 403 TGGTCTCAGCCCCAAGGATCGCGTGGGATGTTTTGAGGCCAAGCCCGCATGTT 462
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 71 TGGTCTCAGCCCCAAGGATCGCGTGGGATGTTTTGAGGCCAAGCCCGCATGTT 130

QY 463 TCTGCGTATCCCAATCACAGACACAGCCGGATGGGAGCCGCTTGGTGGCATCATCT 522
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 131 TCTGCGTATCCCAATCACAGACACAGCCGGATGGGAGCCGCTTGGTGGCATCATCT 190

QY 523 CCTCCAGGACATGATTTTCTCAAGAGAGGAACATGACTGTTTCTTG 572
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 191 CCTCCAGGACATGATTTTCTCAAGAGAGGAACATGACTGTTTCTTG 240

RESULT 27
AAS18240
ID AAS18240 standard; DNA; 10557 BP.
XX
AC AAS18240;
XX
DT 25-FEB-2002 (first entry)
XX
DE Reference sequence for human IMPDH2 gene showing SNPs.
XX
KW Human; single nucleotide polymorphism; SNP; IMPDH2; chromosome 3p21.2;
KW IMP dehydrogenase 2; haplotyping; genotyping; cancer; cytostatic; ds.
XX
OS Homo sapiens.
XX
FH Key
FH variation
FT location/Qualifiers
FT replace (1564, C)
FT /*tag= a
FT /standard name= "Single nucleotide polymorphism"
FT /note= "Polymorphic site 1 (PS1)"
FT replace (1758, T)
FT /*tag= b
FT /standard name= "Single nucleotide polymorphism"
```

FT		/note= "Polymorphic site 2 (PS2)"
FT	variation	replace (1810, T)
FT		/*tag= c
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 3 (PS3)"
FT	variation	replace (1902, C)
FT		/*tag= d
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 4 (PS4)"
FT	exon	1972..2069
FT		/*tag= e
FT		/number= 1
FT	CDS	1972..6937
FT		/*tag= f
FT		/product= "IMPDH2"
FT		/note= "Coding region specifically claimed in
FT		claim 24"
FT	intron	2070..2514
FT		/*tag= g
FT		/number= 1
FT	variation	replace (2511, A)
FT		/*tag= h
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 5 (PS5)"
FT	exon	2515..2563
FT		/*tag= i
FT		/number= 2
FT	intron	2564..2788
FT		/*tag= j
FT		/number= 2
FT	variation	replace (2628, G)
FT		/*tag= k
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 6 (PS6)"
FT	exon	2789..2890
FT		/*tag= l
FT		/number= 3
FT	intron	2891..2997
FT		/*tag= m
FT		/number= 3
FT	exon	2998..3072
FT		/*tag= n
FT		/number= 4
FT	intron	3073..3399
FT		/*tag= o
FT		/number= 4
FT	variation	replace (3294, C)
FT		/*tag= p
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 7 (PS7)"
FT	exon	3400..3606
FT		/*tag= q
FT		/number= 5
FT	variation	replace (3459, C)
FT		/*tag= r
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 8 (PS8)"
FT	intron	3607..4263
FT		/*tag= s
FT		/number= 5
FT	variation	replace (4168, A)
FT		/*tag= t
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 9 (PS9)"
FT	variation	replace (4252, T)
FT		/*tag= u
FT		/standard name= "Single nucleotide polymorphism"
FT		/note= "Polymorphic site 10 (PS10)"
FT	exon	4264..4351
FT		/*tag= v
FT		/number= 6
FT	intron	4352..4424
FT		/*tag= w

```

FT      exon      /number= 6
FT      exon      4425..4624
FT      exon      /tag= x
FT      intron    /number= 7
FT      intron    4625..4701
FT      intron    /tag= y
FT      variation /number= 7
FT      variation replace (4634, C)
FT      variation /tag= z
FT      variation /standard name= "Single nucleotide polymorphism"
FT      variation /note= "Polymorphic site 11 (PS11)"
FT      exon      4702..4792
FT      exon      /tag= aa
FT      intron    /number= 8
FT      intron    4793..4891
FT      intron    /tag= ab
FT      exon      /number= 8
FT      exon      4892..4987
FT      exon      /tag= ac
FT      intron    /number= 9
FT      intron    4988..6052
FT      intron    /tag= ad
FT      exon      /number= 9
FT      exon      6053..6196
FT      exon      /tag= ae
FT      intron    /number= 10
FT      intron    6197..6279
FT      intron    /tag= af
FT      exon      /number= 10
FT      exon      6280..6424
FT      exon      /tag= ag
FT      intron    /number= 11
FT      intron    6425..6518
FT      intron    /tag= ah
FT      intron    /number= 11
FT      intron    replace (6495, T)
FT      variation /tag= ai
FT      variation /standard name= "Single nucleotide polymorphism"
FT      variation /note= "Polymorphic site 12 (PS12)"
FT      exon      6519..6662
FT      exon      /tag= aj
FT      intron    /number= 12
FT      intron    6663..6742
FT      intron    /tag= ak
FT      exon      /number= 12
FT      exon      6743..6826
FT      exon      /tag= al
FT      intron    /number= 13
FT      intron    6827..6915
FT      intron    /tag= am
FT      exon      /number= 13
FT      exon      6916..6937
FT      exon      /tag= an
FT      variation /number= 14
FT      variation replace (7088, T)
FT      variation /tag= ao
FT      variation /standard name= "Single nucleotide polymorphism"
FT      variation /note= "Polymorphic site 13 (PS13)"
PN      WO200177363-A2.
PD      18-OCT-2001.
XX      11-APR-2001; 2001WO-US11851.
PF      11-APR-2000; 2000US-196248P.
XX      11-APR-2000; 2000US-196248P.
XX      (GENA-) GENAISSANCE PHARM INC.
PA      Chew A, Choi JY, Koshy B, Lee HH, Stephens JC;
XX      WPI; 2002-041297/05.
DR      P-PSDB; AAU10695.

```

XX New isolated polynucleotide having polymorphic variant of IMP2
PT dehydrogenase gene, useful for studying expression of the gene in vivo,
PT and for testing efficacy of therapeutic agents for cancer in biological
PT system -
XX
PS Claim 19; Fig 1; 70pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human IMP dehydrogenase 2 (IMPDH2) gene located on
CC chromosome 3p21.2, and methods for haplotyping and/or genotyping the
CC IMPDH2 gene in an individual. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the IMPDH2 gene
CC polymorphisms. The polynucleotides and screened compounds are
CC useful for (developing) treatment of diseases associated with IMPDH2
CC activity, such as cancer. The present sequence represents a reference
CC sequence for the IMPDH2 gene which shows the variations in the gene.
XX
SQ Sequence 10557 BP; 2348 A; 2852 C; 2963 G; 2394 T; 0 other;

Query Match 12.6%; Score 209; DB 24; Length 10557;
Best Local Similarity 100.0%; Pred. NO. 1.6e-89;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 AGAATATGAACAGGATTCATCACAGACCCCTGTGCTCCTCAGCCCC AGATCGCGTGC 429
DB 3398 AGAATATGAACAGGATTCATCACAGACCCCTGTGCTCCTCAGCCCC AGATCGCGTGC 3457
OY 430 GGGATGTTTTGAGCCCAAGCCCCGCGATGTTTCTGCGGTATCCCA TCACAGACACAG 489
DB 3458 GCGATGTTTTGAGGCCAAGCCCCGCGATGTTTCTGCGGTATCCCA TCACAGACACAG 3517
OY 490 GCCGGATGGGAGCCGCTTGTTGGCATCATCTCTCCAGGACATT ATTTCTCAAG 549
DB 3518 GCCGGATGGGAGCCGCTTGTTGGCATCATCTCTCCAGGACATT ATTTCTCAAG 3577
OY 550 AGGAGGAACATGACTGTTTCTTGGAGAG 578
DB 3578 AGGAGGAACATGACTGTTTCTTGGAGAG 3606

RESULT 28
ABV14868
ID ABV14868 standard; cDNA; 379 BP.
XX
AC ABV14868;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 14859.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;

XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 2488; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 379 BP; 87 A; 93 C; 108 G; 91 T; 0 other;

Query Match 9.3%; Score 154; DB 23; Length 379;
Best Local Similarity 100.0%; Pred. NO. 3.2e-63;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1101 GAGTATGCAC3GCGCTTGTGTTCCGGTCATGCTGATGAGGAATCCAAATGTGGGT 1160
DB 225 GAGTATGCAC3GCGCTTGTGTTCCGGTCATGCTGATGAGGAATCCAAATGTGGGT 284
OY 1161 CATATTGCGAAGCCTTGCCCTTGGGCTCCACAGTCATGATGGCTCTCTCTGGCT 1220
DB 285 CATATTGCGAAGCCTTGCCCTTGGGCTCCACAGTCATGATGGCTCTCTCTGGCT 344
OY 1221 GCCACCACCTGAGGCCCTGTGTAATCTTTT 1254
DB 345 GCCACCACCTGAGGCCCTGTGTAATCTTTT 378

RESULT 29
ABV38955
ID ABV38955 standard; cDNA; 437 BP.
XX
AC ABV38955;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 38946.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI

```
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 7915; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 437 BP; 104 A; 114 C; 123 G; 96 T; 0 other;

Query Match          9.3%; Score 153; DB 23; Length 437;
Best Local Similarity 100.0%; Pred. No. 9.6e-63;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1101 GAGTATGCACGGCGCTTGGTGTCCGGTCATTGCTGATGGAGGAATCCAAATGTGGGT 1160
    |||||||
DB 285 GAGTATGCACGGCGCTTGGTGTCCGGTCATTGCTGATGGAGGAATCCAAATGTGGGT 344

QY 1161 CATATTGCGAAGCCTTGCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCTGGCT 1220
    |||||||
DB 345 CATATTGCGAAGCCTTGCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCTGGCT 404

QY 1221 GCCACCACTGAGGCCCTGGTGAATACTTCTTT 1253
    |||||||
DB 405 GCCACCACTGAGGCCCTGGTGAATACTTCTTT 437

RESULT 30
ABV05699
ID ABV05699 standard; cDNA: 389 BP.
XX
AC ABV05699;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 5690.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
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XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 952; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 389 BP; 85 A; 97 C; 114 G; 92 T; 1 other;

Query Match          6.8%; Score 112; DB 23; Length 389;
Best Local Similarity 100.0%; Pred. No. 3.7e-43;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 TGATCAAGTACATCAAGAACAATATCCCTAATCTCCAAGTCATTGGAGCAATGTGTCA 963
    |||||||
DB 28 TGATCAAGTACATCAAGAACAATATCCCTAATCTCCAAGTCATTGGAGCAATGTGTCA 87

QY 964 CTGCTGCCAGGCCAAGACCTCATTTGATGCAAGTGTGGATGCCCTGCCGGT 1015
    |||||||
DB 88 CTGCTGCCAGGCCAAGAACCTCATTTGATGCAAGTGTGGATGCCCTGCCGGT 139

RESULT 31
AAI84483
ID AAI84483 standard; cDNA: 286 BP.
XX
AC AAI84483;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 4543.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
```



```
XX WPI; 2001-514838/56.
DR P-PSDB; AA004552.
XX
PT Isolated nucleic acids and polypeptides, useful for
PT diagnosing and treating e.g. leukaemia, inflammation
PT disorders -
XX
PS Claim 1; SEQ ID NO 4543; 1399pp + Sequence Listing;
XX
CC The invention relates to human polynucleotides (AA17
CC the encoded proteins (AA000010-AA013910) that exhibi
CC cytokine, cell proliferation or cell differentiation
CC production of other cytokines in other cell populati
CC polynucleotides and polypeptides are useful in gene
CC peptide therapy. The polypeptides have various cyto
CC e.g. stem cell growth factor activity, haematopoesi
CC activity, tissue growth factor activity, immunomodul
CC activin/inhibin activity and may be useful in the di
CC treatment of cancer, leukaemia, nervous system disor
CC inflammation.
CC Note: The sequence data for this patent did not form
CC specification, but was obtained in electronic format
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 286 BP; 78 A; 79 C; 60 G; 69 T; 0 other;

Query Match          4.2%; Score 69; DB 22; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 GATGGCCATGCAATGGCGTTACAGGCGTATTTGGCTTCATCCACC CAACTGTACACC 337
   |||||||
DB 157 GATGGCCATGCAATGGCGTTACAGGCGTATTTGGCTTCATCCACC CAACTGTACACC 216
QY 338 TGAATTCCA 346
   |||||||
DB 217 TGAATTCCA 225

RESULT 32
AA003541
ID AA003541 standard; DNA; 1620 BP.
XX
AC AA003541;
XX
DT 31-AUG-1990 (first entry)
XX
DE Chinese hamster IMPDH.
XX
KW Inosine 5'-mono-phosphate dehydrogenase; hepatomas;
KW guanosine monophosphate; ss.
XX
OS Cricetulus sp.
XX
PN WO9001545-A.
XX
PD 22-FEB-1990.
XX
PF 02-AUG-1989; 89WO-0000344.
XX
PR 12-AUG-1988; 88US-0232302.
XX
PA (ARCH-) ARCH. DEV. CORP.
XX
PI Collart FR, Huberman E;
XX
DR WPI; 1990-083504/11.
DR N-PSDB; AA003541.
XX
PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
PT used to detect high levels of enzyme activity of tumour cells,
PT esp. hepatomas, and to produce guanosine monophosphate.
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XX Claim 8; Fig 2; 51pp; English.
PS
XX
CC The sequence can be used to quantitatively detect IMPDH encoding
CC DNA or RNA by hybridisation, eg in normal and malignant cells,
CC esp. hepatomas.
CC See also AA003540.
XX
SQ Sequence 1620 BP; 423 A; 369 C; 421 G; 406 T; 1 other;

Query Match          3.7%; Score 62; DB 11; Length 1620;
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 GGTATTGGCTTCATCCACCACCACTGTACAGCTGAATTCCAGGCCAATGAAGTTCGAAA 365
   |||||||
DB 284 GGTATTGGCTTCATCCACCACCACTGTACAGCTGAATTCCAGGCCAATGAAGTTCGAAA 343
QY 366 GT 367
   ||
DB 344 GT 345

RESULT 33
ABN32859
ID ABN32859 standard; DNA; 60 BP.
XX
AC ABN32859;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:5607.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 5607; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
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CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 17 A; 17 C; 14 G; 12 T; 0 other;

Query Match 3.6%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 GACAAATACCCCTAATCTCCAAAGTCATTGGAGGCAATGTGTCACCTGCTGCCAGGCCAAG 980
|||||
Db 1 GACAAATACCCCTAATCTCCAAAGTCATTGGAGGCAATGTGTCACCTGCTGCCAGGCCAAG 60

RESULT 34
AAH90485/c
ID AAH90485 standard; cDNA; 51 BP.
XX
AC AAH90485;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human clone cg43922096 SNP site, SEQ ID NO:365.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 3p24.2;
KW detection; identification; gene therapy; genetic disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(25..27,GC)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200147942-A2.
XX
PD 05-JUL-2001.
XX
PE 27-DEC-2000; 2000WO-US35387.
XX
PR 27-DEC-1999; 99US-0472865.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-425617/45.
XX
XX

PT New polynucleotides containing single nucleotide polymorphisms, for
PT detecting the presence of polymorphism, detecting a polymorphic site,
PT and treating a patient suffering from a pathology ascribed to the
PT polymorphism -
XX
XX

PS Claim 1; Page 99; 295pp; English.

CC Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs
CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino
CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)
CC result in non-conservative changes. The SNP in sequences 579 and 580

CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic proteins/
CC peptides using the antibodies. The nucleic acids are useful for gene
CC therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
XX
SQ Sequence 51 BP; 12 A; 20 C; 13 G; 6 T; 0 other;

Query Match 3.1%; Score 51; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CGGCGGTGCCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGGCAG 77
|||||
Db 51 CGGCGGTGCCTGTGTGGCCATGGCCGACTACCTGATTAGTGGGGCAGC 1

RESULT 35
AAT25471
ID AAT25471 standard; cDNA to mRNA; 50 BP.
XX
AC AAT25471;
XX
DT 17-OCT-1996 (first entry)
XX
DE Human gene signature HUMGS07638.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
OS Homo sapiens.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PE 11-NOV-1994; 94WO-JP01916.
XX
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
XX

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
XX

PS Claim 1; Page 1838; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in AAT19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be

CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX
SQ Sequence 50 BP; 17 A; 10 C; 7 G; 16 T; 0 other;

Query Match 2.9%; Score 48; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1598 GATCCAGCACACTCTCGGTTTTCATTAAGTTAGAAAG 1645
Db 1 GATCCAGCACACTCTCGGTTTTCATTAAGTTAGAAAG 48

RESULT 36
ABK40085
ID ABK40085 standard; DNA; 6193 BP.
XX
AC ABK40085;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human chemically pretreated gene sequence #84 strand 1.
XX
KW Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
KW cytosstatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1;
KW UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200202806-A2.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-EP07470.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-154757/20.
XX
XX
PT New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers,
PT useful for detecting cytosine methylation state of genes associated
PT with pharmacogenomics and for therapy of diseases e.g. cancer -
XX
XX
PS Claim 1; SEQ ID No 167; 24pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence at
CC least 18 bases in length of a segment of the chemically pretreated DNA
CC of genes associated with pharmacogenomics according to one of the
CC sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B1
CC (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2
CC (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360),
CC MRP (NM_004996, NM_019900, NM_019901, NM_019902, NM_019862, NM_019898,
CC NM_019899) and their complementary sequences, or a sequence (SI) chosen
CC from 87 sequences and their complements. The chemical pretreatment
CC is bisulphite treatment to convert cytosines (but not methyl-cytosines)
CC into uracils. Also included are an oligomer (II) in particular an
CC oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in
CC each case at least one base sequence having a length of 9 nucleotides
CC which hybridises to or is identical to a chemically pretreated DNA of
CC genes associated with pharmacogenomics and their complements, arranged in
CC an array for analysing diseases associated with the methylation state
CC (CpG) and/or detecting SNPs (single nucleotide polymorphisms)
CC of the 87 sequences. The oligomers may also be used as PCR primers.
CC The set of 87 nucleic acids and their complements is useful for diagnosis
CC and therapy of solid tumours and cancer. The present sequence
CC represents one the 87 DNA sequences or its complement

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6193 BP; 1404 A; 124 C; 1628 G; 3037 T; 0 other;

Query Match 1.7%; Score 28; DB 24; Length 6193;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 AAGGATCGCGTGGGATGTTTGGAG 444
Db 2561 AAGGATCGCGTGGGATGTTTGGAG 2588

RESULT 37
AAH90486/c
ID AAH90486 standard; cDNA; 50 BP.
XX
AC AAH90486;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human clone cg43922096 SNP site, SEQ ID NO:366.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 3p24.2;
KW detection; identification; gene therapy; genetic disorder; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FH variation replace(25..26,GCC)
FT /*tag= a
FT /*standard_name= "single nucleotide polymorphism"
XX
PN WO200147942-A2.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-US35387.
XX
PR 27-DEC-1999; 99US-0472865.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-425617/45.
XX
XX
PT New polynucleotides containing single nucleotide polymorphisms, for
PT detecting the presence of polymorphism, detecting a polymorphic site,
PT and treating a patient suffering from a pathology ascribed to the
PT polymorphism -
XX
XX
PS Claim 1; Page 95; 295pp; English.
XX
CC Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs
CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino
CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)
CC result in non-conservative changes. The SNP in sequences 579 and 580
CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic proteins/
CC peptides using the antibodies. The nucleic acids are useful for gene
CC therapy of an individual having, suspected of having, or at risk of

CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
XX
SQ Sequence 50 BP; 12 A; 20 C; 12 G; 6 T; 0 other;

Query Match 1.6%; Score 26; DB 22; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CGCGGTGTCCTGTGTGGCCATGGC 52
|||||
Db 50 CGCGGTGTCCTGTGTGGCCATGGC 25

RESULT 38
AAH90484/c
ID AAH90484 standard; cDNA; 51 BP.

XX
AC AAH90484;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human clone cg43922096 SNP site, SEQ ID NO:364.
XX

KW Human; single nucleotide polymorphism; SNP; chromosome 3p24.2;
KW detection; identification; gene therapy; genetic disorder; ss.
XX
OS Homo sapiens.

FH Key location/Qualifiers
FT variation replace(26,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

XX
PN WO200147942-A2.

XX
PD 05-JUL-2001.

XX
PF 27-DEC-2000; 2000WO-US35387.

XX
PR 27-DEC-1999; 99US-0472865.

XX
PA (CURA-) CURAGEN CORP.

XX
PI Shimkets RA, Leach M;

XX
DR WPI; 2001-425617/45.

XX
PT New polynucleotides containing single nucleotide polymorphisms, for
PT detecting the presence of polymorphism, detecting a polymorphic site,
PT and treating a patient suffering from a pathology ascribed to the
PT polymorphism -

XX
PS Claim 1; Page 99; 295pp; English.

XX
CC Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs
CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino
CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)
CC result in non-conservative changes. The SNP in sequences 579 and 580
CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic proteins/
CC peptides using the antibodies. The nucleic acids are useful for gene
CC therapy of an individual having, suspected of having, or at risk of

CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
XX

SQ Sequence 51 BP; 6 A; 18 C; 12 G; 15 T; 0 other;

Query Match 1.6%; Score 26; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 AGAGGAAGACTTGTTGTAGCCCC 614
|||||
Db 51 AGAGGAAGACTTGTTGTAGCCCC 26

RESULT 39
AAD28933/c
ID AAD28933 standard; DNA; 35 BP.

XX
AC AAD28933;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human wild-type, type II IMPDH cDNA amplifying 3' primer.
XX

KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW therapy; PCR primer; ss.
XX
OS Homo sapiens.

XX
PN WO200185952-A2.
XX
PD 15-NOV-2001.

XX
PF 10-MAY-2001; 2001WO-US15457.

XX
PR 10-MAY-2000; 2000US-203448P.

XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX
PI Krystek SR, Sheriff S, Witmer MR, Hollenbaugh DL, Yan N;

XX
PI Mouravieff JE, Einspahr HM, Kish K;

XX
DR WPI; 2002-164105/21.

XX
PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies -

XX
PS Example 1; Page 56; 161pp; English.

XX
CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or
CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other
CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the
CC management of cancer or other proliferative-type diseases, and in
CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is a PCR primer used to amplify human wild-type, type II
CC IMPDH cDNA.

SQ Sequence 35 BP; 10 A; 9 C; 7 G; 9 T; 0 other;

Query Match 1.5%; Score 25; DB 24; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1570 CGTATGAGAACGGCTTTCTGAAA 1594
|||||
DB 35 CGTATGAGAACGGCTTTCTGAAA 11

RESULT 40

AAH90483/c
ID AAH90483 standard; cDNA; 51 BP.

XX AC AAH90483;

DT 08-OCT-2001 (first entry)

DE Human clone cg43922096 SNP site, SEQ ID NO:363.

KW Human; single nucleotide polymorphism; SNP; chromosome 3p24.2;
KW detection; identification; gene therapy; genetic disorder; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT variation replace(26,G)
FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

PN WO200147942-A2.

PD 05-JUL-2001.

PF 27-DEC-2000; 2000WO-US35387.

PR 27-DEC-1999; 99US-0472865.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-425617/45.

PT New polynucleotides containing single nucleotide polymorphisms, for
PT detecting the presence of polymorphism, detecting a polymorphic site,
PT and treating a patient suffering from a pathology ascribed to the
PT polymorphism -

PS Claim 1; Page 99; 295pp; English.

XX Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs
CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino
CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)
CC result in non-conservative changes. The SNP in sequences 579 and 580
CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic proteins/
CC peptides using the antibodies. The nucleic acids are useful for gene
CC therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
SQ Sequence 51 BP; 7 A; 18 C; 11 G; 15 T; 0 other;

Query Match 1.5%; Score 25; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 AGAGGGAAGACTTGTTGGTAGCCCC 613
|||||
DB 51 AGAGGGAAGACTTGTTGGTAGCCCC 27

RESULT 41

AAA30019/c
ID AAA30019 standard; DNA; 27 BP.

XX AC AAA30019;

DT 09-AUG-2000 (first entry)

DE Hairpin hybridizer molecule #24 targeting c-ras and IMPDH RNA.

KW DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW c-ras; inhibitor; detect; nuclease resistance; gene function; IMPDH;
KW gene expression modulator; inosine 5-monophosphate dehydrogenase; ss.

OS Synthetic.

FH Key Location/Qualifiers
FT misc_RNA 1..7
FT /*tag= a

FT /note= "2-O-methyl ribonucleotides"

FT stem_loop 1..27
FT /*tag= b

FT misc_feature 8..17
FT /*tag= c

FT /note= "Phosphorothioate internucleotide linkage"

FT misc_RNA 17..27
FT /*tag= d

FT /note= "2-O-methyl ribonucleotides"

PN WO200017346-A2.

PD 30-MAR-2000.

PF 20-SEP-1999; 99WO-US21865.

PR 21-SEP-1998; 98US-0101174.

PA (RIBO-) RIBOZYME PHARM INC.

PI Hartmann T, Zwick M, Thompson J, Jarvis T;

DR WPI; 2000-292841/25.

PT Modulating target sequence in a cell, useful e.g. therapeutically or
PT for identifying gene function, by treatment with novel hairpin
PT hybridizer nucleic acid molecules -

PS Claim 101; Page 77; 128pp; English.

XX A method for modulating the function of a target sequence in a cell
CC comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC such as that represented by the present sequence. The present HPH
CC molecule is used in an example of the invention and targets the human
CC c-ras and inosine 5-monophosphate dehydrogenase (IMPDH) RNA. The HPH
CC molecules function through RNA/DNA inhibition. The HPH molecule binds to
CC and blocks the function of a target nucleic acid, and modulated cellular
CC and viral processes such as splicing, editing, and translation. The HPH
CC molecule can be used therapeutically, in target validation, to identify
CC gene function and/or therapeutic targets, for analysis of mutations in
CC diseased cell and to detect specific RNA. The hairpin structure improves
CC resistance to nuclease degradation, localization within the cell, and
CC uptake by cells. The HPH may include a sequence that activates RNase H
CC (for cleaving RNA) and its specificity is greater than for linear
CC antisense sequences.

```

XX SQ      Sequence 27 BP; 7 A; 9 C; 5 G; 3 T; 3 U; 0 other;
      Query Match
      Best Local Similarity 100.0%; Score 24; DB 21; Length 27;
      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 764 TGCCAAGAAACAGCTGCTGTGTGG 787
Db 24 TGCCAAGAAACAGCTGCTGTGTGG 1

RESULT 42
AAA30020/c
ID AAA30020 standard; DNA; 29 BP.
XX AC      AAA30020;
XX DT      09-AUG-2000 (first entry)
XX DE      Hairpin hybridizer molecule #25 targeting c-raf and IMPDH RNA.
XX KW      DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
XX KW      c-raf; inhibitor; detect; nuclease resistance; gene function; IMPDH;
XX KW      gene expression modulator; inosine 5'-monophosphate dehydrogenase; ss.
XX OS      Synthetic.
XX FH      Key
XX FT      misc_RNA
XX FT      Location/Qualifiers
XX FT      1..7
XX FT      /tag= a
XX FT      /note= "2-O-methyl ribonucleotides"
XX FT      stem_loop
XX FT      1..29
XX FT      /tag= b
XX FT      misc_feature
XX FT      8..17
XX FT      /tag= c
XX FT      /note= "phosphorothioate internucleotide linkage"
XX FT      17..29
XX FT      /tag= d
XX FT      /note= "2-O-methyl ribonucleotides"
XX PN      WO200017346-A2.
XX PD      30-MAR-2000.
XX PE      20-SEP-1999; 99WO-US21865.
XX PR      21-SEP-1998; 98US-0101174.
XX PA      (RIBO-) RIBOZYME PHARM INC.
XX PI      Hartmann T, Zwick M, Thompson J, Jarvis T;
XX DR      WPI; 2000-292841/25.
XX PT      Modulating target sequence in a cell, useful e.g. therapeutically or
XX PT      for identifying gene function, by treatment with novel hairpin
XX PT      hybridizer nucleic acid molecules
XX PS      Claim 101; Page 77; 128pp; English.
XX CC      A method for modulating the function of a target sequence in a cell
XX CC      comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
XX CC      such as that represented by the present sequence. The present HPH
XX CC      molecule is used in an example of the invention and targets the human
XX CC      c-raf and inosine 5-monophosphate dehydrogenase (IMPDH) RNA. The HPH
XX CC      molecules function through RNA/DNA inhibition. The HPH molecule binds to
XX CC      and blocks the function of a target nucleic acid, and modulated cellular
XX CC      and viral processes such as splicing, editing, and translation. The HPH
XX CC      molecule can be used therapeutically, in target validation, to identify
XX CC      gene function and/or therapeutic targets, for analysis of mutations in
XX CC      diseased cell and to detect specific RNA. The hairpin structure improves
XX CC      resistance to nuclease degradation, localization within the cell, and
```

```

CC CC      uptake by cells. The HPH may include a sequence that activates RNase H
CC CC      (for cleaving RNA) and its specificity is greater than for linear
CC CC      antisense sequences.
XX SQ      Sequence 29 BP; 7 A; 10 C; 6 G; 3 T; 3 U; 0 other;
      Query Match
      Best Local Similarity 100.0%; Score 24; DB 21; Length 29;
      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 764 TGCCAAGAAACAGCTGCTGTGTGG 787
Db 24 TGCCAAGAAACAGCTGCTGTGTGG 1

RESULT 43
AAD28932
ID AAD28932 standard; DNA; 33 BP.
XX AC      AAD28932;
XX DT      07-MAY-2002 (first entry)
XX DE      Human wild-type, type II IMPDH cDNA amplifying 5' primer.
XX KW      Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
XX KW      proliferative-type disease; cancer; imaging methodology; cytostatic;
XX KW      therapy; PCR primer; ss.
XX OS      Homo sapiens.
XX PN      WO200185952-A2.
XX PD      15-NOV-2001.
XX PF      10-MAY-2001; 2001WO-US15457.
XX PR      10-MAY-2000; 2000US-203448P.
XX PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI      Krystek SR, Sherliff S, Wilmer MR, Hollenbaugh DL, Yan N;
XX PI      Mouravieff JE, Einspahr HM, Kish K;
XX DR      WPI; 2002-164105/21.
XX PT      New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
XX PT      having an oligo-peptide domain substituted for a subdomain of a
XX PT      wild-type IMPDH polypeptide, useful in drug discovery or for generating
XX PT      antibodies
XX PS      Example 1; Page 56; 161pp; English.
XX CC      The invention relates to modified inosine 5'-monophosphate dehydrogenase
XX CC      (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
XX CC      substituted for a subdomain of a wild-type IMPDH polypeptide. The
XX CC      modified IMPDH polypeptides are useful for drug discovery, for
XX CC      therapeutic, diagnostic and prognostic procedures for detecting or
XX CC      quantifying modified IMPDH polypeptides and their corresponding related
XX CC      acids. IMPDH polypeptides are also useful for generating antibodies, as
XX CC      diagnostic and prognostic markers of diseases, as targets for various
XX CC      therapeutic modalities, and to identify and isolate ligands and other
XX CC      agents that bind to modified IMPDH. These antibodies may be used in
XX CC      diagnostic assays, imaging methodologies, therapeutic methods in the
XX CC      management of cancer or other proliferative-type diseases, and in
XX CC      purifying modified IMPDH polypeptides and for isolating related
XX CC      molecules such as wild type and mutant IMPDH polypeptides. The present
XX CC      sequence is a PCR primer used to amplify human wild-type, type II
XX CC      IMPDH cDNA.
XX SQ      Sequence 33 BP; 7 A; 8 C; 9 G; 9 T; 0 other;
      Query Match
      1.5%; Score 24; DB 24; Length 33;
```

Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGCCGACTACTGATTAGTGGG 71
|||||
Db 10 ATGCCGACTACTGATTAGTGGG 33

RESULT 44
AAA30021/c
ID AAA30021 standard; DNA; 23 BP.

AC AAA30021;
DT 09-AUG-2000 (first entry)

DE Hairpin hybridizer molecule #24 targeting c-raf and MPDH RNA.

KW DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW c-raf; inhibitor; detect; nuclease resistance; gene function; IMPDH;
KW gene expression modulator; inosine 5-monophosphate d dehydrogenase; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT misc_RNA 1..7

FT /tag= a
/note= "2-O-methyl ribonucleotides"

FT stem_loop 1..23

FT misc_feature 8..17

FT /tag= c
/note= "Phosphorothioate internucleotide linkage"

FT misc_RNA 17..23

FT /tag= d
/note= "2-O-methyl ribonucleotides"

PN WO200017346-A2.

PD 30-MAR-2000.

PF 20-SEP-1999; 99WO-US21865.

PR 21-SEP-1998; 98US-0101174.

PA (RIBO-) RIBOZYME PHARM INC.

PI Hartmann T, Zwick M, Thompson J, Jarvis T;

DR WPI; 2000-292841/25.

PT Modulating target sequence in a cell, useful e.g. therapeutically or
PT for identifying gene function, by treatment with novel hairpin
PT hybridizer nucleic acid molecules -

XX Example 6; Page 77; 128pp; English.

CC A method for modulating the function of a target sequence in a cell
CC comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC such as that represented by the present sequence. The present HPH
CC molecule is used in an example of the invention and targets the human
CC c-raf and inosine 5-monophosphate dehydrogenase (IMPDH) RNA. The HPH
CC molecules function through RNA/DNA inhibition. The HPH molecule binds to
CC and blocks the function of a target nucleic acid, and modulated cellular
CC and viral processes such as splicing, editing, and translation. The HPH
CC molecule can be used therapeutically, in target validation, to identify
CC gene function and/or therapeutic targets, for analysis of mutations in
CC diseased cell and to detect specific RNA. The hairpin structure improves
CC resistance to nuclease degradation, localization within the cell, and
CC uptake by cells. The HPH may include a sequence that activates RNase H
CC (for cleaving RNA) and its specificity is greater than for linear
CC antisense sequences.

SQ Sequence 23 BP; 1 A; 6 C; 9 G; 3 T; 4 U; 0 other;

Query Match 1.48; Score 23; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CGACGGACTCACAGCAGCAGC 114
|||||
Db 23 CGACGGACTCACAGCAGCAGC 1

RESULT 45
AAA30022/c
ID AAA30022 standard; DNA; 27 BP.

AC AAA30022;

DT 09-AUG-2000 (first entry)

DE Hairpin hybridizer molecule #27 targeting c-raf and IMPDH RNA.

KW DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW c-raf; inhibitor; detect; nuclease resistance; gene function; IMPDH;
KW gene expression modulator; inosine 5-monophosphate dehydrogenase; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT misc_RNA 1..7

FT /tag= a
/note= "2-O-methyl ribonucleotides"

FT stem_loop 1..27

FT /tag= b
/tag= c

FT /note= "Phosphorothioate internucleotide linkage"

FT misc_RNA 17..27

FT /tag= d
/note= "2-O-methyl ribonucleotides"

PN WO200017346-A2.

PD 30-MAR-2000.

PF 20-SEP-1999; 99WO-US21865.

PR 21-SEP-1998; 98US-0101174.

PA (RIBO-) RIBOZYME PHARM INC.

PI Hartmann T, Zwick M, Thompson J, Jarvis T;

DR WPI; 2000-292841/25.

PT Modulating target sequence in a cell, useful e.g. therapeutically or
PT for identifying gene function, by treatment with novel hairpin
PT hybridizer nucleic acid molecules -

XX Claim 101; Page 77; 128pp; English.

CC A method for modulating the function of a target sequence in a cell
CC comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC such as that represented by the present sequence. The present HPH
CC molecule is used in an example of the invention and targets the human
CC c-raf and inosine 5-monophosphate dehydrogenase (IMPDH) RNA. The HPH
CC molecules function through RNA/DNA inhibition. The HPH molecule binds to
CC and blocks the function of a target nucleic acid, and modulated cellular
CC and viral processes such as splicing, editing, and translation. The HPH
CC molecule can be used therapeutically, in target validation, to identify
CC gene function and/or therapeutic targets, for analysis of mutations in
CC diseased cell and to detect specific RNA. The hairpin structure improves
CC resistance to nuclease degradation, localization within the cell, and
CC uptake by cells. The HPH may include a sequence that activates RNase H

CC (for cleaving RNA) and its specificity is greater than for linear
CC antisense sequences.
XX
SQ Sequence 27 BP; 2 A; 8 C; 9 G; 3 T; 5 U; 0 other;
Query Match 1.4%; Score 23; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 92 CGACGACTCACACACAGCAGC 114
Db 23 CGACGACTCACACACAGCAGC 1
RESULT 46
AAA30006/c
ID AAA30006 standard; DNA; 29 BP.
XX
AC AAA30006;
XX
DT 09-AUG-2000 (first entry)
XX
DE Hairpin hybridizer molecule #11 targeting c-raf and IMPDH RNA.
XX
KW DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW c-raf; inhibitor; detect; nuclease resistance; gene function; IMPDH;
KW gene expression modulator; inosine 5-monophosphate dehydrogenase; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT stem_loop 1..29
FT /*tag= a
FT misc_RNA 1..7
FT /*tag= b
FT /*note= "2'-O-methyl-ribonucleotides"
FT misc_feature 1..4
FT /*tag= c
FT /*note= "phosphorothioate internucleotide linkage"
FT misc_feature 8..17
FT /*tag= d
FT /*note= "Phosphorothioate internucleotide linkage"
FT misc_RNA 17..29
FT /*tag= e
FT /*note= "2'-O-methyl-ribonucleotides"
FT misc_feature 26..29
FT /*tag= f
FT /*note= "phosphorothioate internucleotide linkage"
XX
PN WO200017346-A2.
XX
PD 30-MAR-2000.
XX
PF 20-SEP-1999; 99WO-US21865.
XX
PR 21-SEP-1998; 98US-0101174.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Hartmann T, Zwick M, Thompson J, Jarvis T;
XX
DR WPI; 2000-292841/25.
XX
PT Modulating target sequence in a cell, useful e.g. therapeutically or
PT for identifying gene function, by treatment with novel hairpin
PT hybridizer nucleic acid molecules -
XX
PS Claim 3; Page 77; 128pp; English.
XX
CC A method for modulating the function of a target sequence in a cell
CC comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC such as that represented by the present sequence. The present HPH
CC molecule is used in an example of the invention and targets the human

CC c-raf and inosine 5-monophosphate dehydrogenase (IMPDH) RNA. The HPH
CC molecules function through RNA/DNA inhibition. The HPH molecule binds to
CC and blocks the function of a target nucleic acid, and modulated cellular
CC and viral processes such as splicing, editing, and translation. The HPH
CC molecule can be used therapeutically, in target validation, to identify
CC gene function and/or therapeutic targets, for analysis of mutations in
CC diseased cell and to detect specific RNA. The hairpin structure improves
CC resistance to nuclease degradation, localization within the cell, and
CC uptake by cells. The HPH may include a sequence that activates RNase H
CC (for cleaving RNA) and its specificity is greater than for linear
CC antisense sequences.
XX
SQ Sequence 29 BP; 4 A; 8 C; 9 G; 3 T; 5 U; 0 other;
Query Match 1.4%; Score 23; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 765 GCCAAGAAACAGCTGCTGTGTGG 787
Db 23 GCCAAGAAACAGCTGCTGTGTGG 1
RESULT 47
AAA30023/c
ID AAA30023 standard; DNA; 29 BP.
XX
AC AAA30023;
XX
DT 09-AUG-2000 (first entry)
XX
DE Hairpin hybridizer molecule #28 targeting c-raf and IMPDH RNA.
XX
KW DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW c-raf; inhibitor; detect; nuclease resistance; gene function; IMPDH;
KW gene expression modulator; inosine 5-monophosphate dehydrogenase; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1..7
FT /*tag= a
FT /*note= "2-O-methyl ribonucleotides"
FT stem_loop 1..29
FT /*tag= b
FT misc_feature 8..17
FT /*tag= c
FT /*note= "Phosphorothioate internucleotide linkage"
FT misc_RNA 17..29
FT /*tag= d
FT /*note= "2-O-methyl ribonucleotides"
XX
PN WO200017346-A2.
XX
PD 30-MAR-2000.
XX
PF 20-SEP-1999; 99WO-US21865.
XX
PR 21-SEP-1998; 98US-0101174.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Hartmann T, Zwick M, Thompson J, Jarvis T;
XX
DR WPI; 2000-292841/25.
XX
PT Modulating target sequence in a cell, useful e.g. therapeutically or
PT for identifying gene function, by treatment with novel hairpin
PT hybridizer nucleic acid molecules -
XX
PS Claim 101; Page 77; 128pp; English.
XX
CC A method for modulating the function of a target sequence in a cell

CC comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC such as that represented by the present sequence. The present HPH
CC molecule is used in an example of the invention and targets the human
CC c-raf and inosine 5'-monophosphate dehydrogenase (IMPDH) RNA. The HPH
CC molecules function through RNA/DNA inhibition. The HPH molecule binds to
CC and blocks the function of a target nucleic acid, and modulated cellular
CC and viral processes such as splicing, editing, and translation. The HPH
CC molecule can be used therapeutically, in target validation, to identify
CC gene function and/or therapeutic targets, for analysis of mutations in
CC diseased cell and to detect specific RNA. The hairpin structure improves
CC resistance to nuclease degradation, localization within the cell, and
CC uptake by cells. The HPH may include a sequence that activates RNase H
CC (for cleaving RNA) and its specificity is greater than for linear
CC antisense sequences.

SO Sequence 29 BP; 3 A; 9 C; 9 G; 3 T; 5 U; 0 other;

Query Match 1.4%; Score 23; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 CGACGACTCACAGCAGCAGC 114
DB 23 CGACGACTCACAGCAGCAGC 1

RESULT 48
AAD28935/C

ID AAD28935 standard; DNA: 30 BP.

AC AAD28935;

DT 07-MAY-2002 (first entry)

DE Human type II DKT-IMPDH cDNA amplifying 3' primer.

KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW therapy; PCR primer; ss.

OS Homo sapiens.

PN WO200185952-A2.

PD 15-NOV-2001.

PF 10-MAY-2001; 2001WO-US15457.

PR 10-MAY-2000; 2000US-203448P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Krystek SR, Sheriff S, Witmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;

DR WPI; 2002-164105/21.

PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies

PS Example 1; Page 57; 161pp; English.

CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or
CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other

CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the
CC management of cancer or other proliferative-type diseases, and in
CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is a PCR primer used to amplify human type II DKT-IMPDH cDNA.
XX

SO Sequence 30 BP; 5 A; 8 C; 4 G; 13 T; 0 other;

Query Match 1.4%; Score 23; DB 24; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 357 GTTCGAAAGTGAAGAATATGA 379
DB 30 GTTCGAAAGTGAAGAATATGA 8

RESULT 49

AAD28937/C
ID AAD28937 standard; DNA: 30 BP.

AC AAD28937;

DT 07-MAY-2002 (first entry)

DE Human type II GSG-IMPDH cDNA amplifying 3' primer.

KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW therapy; PCR primer; ss.

OS Homo sapiens.

PN WO200185952-A2.

PD 15-NOV-2001.

PF 10-MAY-2001; 2001WO-US15457.

PR 10-MAY-2000; 2000US-203448P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Krystek SR, Sheriff S, Witmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;

DR WPI; 2002-164105/21.

PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies

PS Example 1; Page 57; 161pp; English.

CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or
CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other
CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the
CC management of cancer or other proliferative-type diseases, and in
CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is a PCR primer used to amplify human type II GSG-IMPDH cDNA.
XX

SO Sequence 30 BP; 7 A; 10 C; 4 G; 9 T; 0 other;

Query Match 1.3%; Score 22; DB 24; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 12, 2003, 23:43:00
Job time : 374 secs

OY 357 GTTCGGAAGTGAGAAATATG 378
|||||
Db 30 GTTCGGAAGTGAGAAATATG 9

RESULT 50
AAD28939/c
ID AAD28939 standard; DNA: 33 BP.
XX
AC AAD28939;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human type II AGRP-IMPDH cDNA amplifying 3' primer.
XX
KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200185952-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US15457.
XX
PR 10-MAY-2000; 2000US-203448P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Krystek SR, Sheriff S, Wiltner MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;
XX
DR WPI; 2002-164105/21.
XX
XX
PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies
XX
XX
PS Example 1; Page 58; 161pp; English.
XX
XX
CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC modified IMPDH polypeptides are useful for drug discovery, for
CC therapeutic, diagnostic and prognostic procedures for detecting or
CC quantifying modified IMPDH polypeptides and their corresponding nucleic
CC acids. IMPDH polypeptides are also useful for generating antibodies, as
CC diagnostic and prognostic markers of diseases, as targets for various
CC therapeutic modalities, and to identify and isolate ligands and other
CC agents that bind to modified IMPDH. These antibodies may be used in
CC diagnostic assays, imaging methodologies, therapeutic methods in the
CC management of cancer or other proliferative-type diseases, and in
CC purifying modified IMPDH polypeptides and for isolating related
CC molecules such as wild type and mutant IMPDH polypeptides. The present
CC sequence is a PCR primer used to amplify human type II AGRP-IMPDH cDNA.
XX
SQ Sequence 33 BP; 8 A; 11 C; 5 G; 9 T; 0 other;

Query Match 1.3%; Score 22; DB 24; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 357 GTTCGGAAGTGAGAAATATG 378
|||||
Db 33 GTTCGGAAGTGAGAAATATG 12

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2003, 15:05:49 ; Search time 837 Seconds
(without alignments)
11052.834 Million cell updates/sec

Title: US-09-846-637C-3
Perfect score: 1654
Sequence: 1 gaattcggcgcgtccctcgga.....gtttagaagaaccgcgaattc 1654

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/A2001B.DAT:*
24: /SIDS2/gcgcdata/geneseq/geneseqn-emb1/A2002.DAT:*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1635.6	98.9	1642	11	AAQ03540	Human IMPDH cDNA.
2	1621.4	98.0	2277	23	ABV29489	Human prostate exp
3	1475	89.2	1677	23	ABV23631	Human prostate exp
4	1475	89.2	1677	23	ABV24746	Human prostate exp
5	1449.4	87.6	1905	20	AAZ41300	Human normal ovari
6	1320.2	79.8	1620	11	AAQ03541	Chinese hamster IM
7	1236.8	74.8	2019	21	AAF21634	Human breast and o
8	1141.6	69.0	1157	24	ABK34910	Human cDNA encodin
9	960.8	58.1	2858	24	ABK83782	Human cDNA differe

10	960.8	58.1	2858	24	ABN95621	Gene #2119 used to
11	865.6	52.3	3387	23	AAS86456	DNA encoding novel
12	816.4	49.4	1158	24	AAD28929	Human type II IMPD
13	813.2	49.2	1158	24	AAD28927	Human type II IMPD
14	810	49.0	1158	24	AAD28928	Human type II IMPD
15	809.6	48.9	1155	24	AAD28922	Human type II IMPD
16	809.6	48.9	1155	24	AAD28923	Human type II IMPD
17	809.6	48.9	1155	24	AAD28924	Human type II IMPD
18	809.6	48.9	1155	24	AAD28925	Human type II IMPD
19	769.2	46.5	38358	22	AAK73535	Human immune/haema
20	602.6	36.4	2498	23	ABL17903	Drosophila melanog
21	602.6	36.4	2908	23	ABL03461	Drosophila melanog
22	583.6	35.3	607	23	ABV44742	Human prostate exp
23	545.6	33.0	674	21	AAF18367	Lung cancer associ
24	513.6	31.1	1155	24	AAD28926	Human type I IMPDH
25	484.2	29.3	554	21	AAC03976	Human secreted pro
26	439	26.5	558	24	ABO58310	Human colon cancer
27	420.6	25.4	675	21	AAZ80760	Human colon cancer
28	410.2	24.8	3616	20	AAK78081	A. gossypii GUAl D
29	404.6	24.5	1297	23	AAS87918	DNA encoding novel
30	396	23.9	396	22	AAF94973	Human ovarian canc
31	396	23.9	396	24	ABT03240	Human ovarian carc
32	396	23.9	396	24	ABL48923	Ovarian carcinoma
33	383	23.2	1453	21	AAF13369	Aspergillus oryzae
34	362.4	21.9	1712	22	AAH29715	S cerevisiae apopt
35	341.4	20.6	379	23	ABV14868	Human prostate exp
36	340.4	20.6	437	23	ABV38955	Human prostate exp
37	328.8	19.9	6193	24	ABN95699	Gene #2197 used to
38	314.2	19.0	577	24	ABO59475	Human colon cancer
39	310.4	18.8	420	23	ABV37312	Human prostate exp
40	303	18.3	1734	21	AAC47444	Arabidopsis thalia
41	303	18.3	1736	21	AAC39104	Arabidopsis thalia
42	295.6	17.9	1509	21	AAC42828	Arabidopsis thalia
43	270.6	16.4	286	22	AAI84483	Human polynucleoti
44	267.6	16.2	391	23	ABV07378	Human prostate exp
45	255.6	15.5	1470	23	AAS54218	Pseudomonas aerugi

ALIGNMENTS

RESULT 1	AAQ03540	standard; cDNA; 1642 BP.
ID	AAQ03540;	
AC	AAQ03540;	
XX		
DT	31-AUG-1990	(first entry)
XX		
DE	Human IMPDH cDNA.	
XX		
KW	Inosine 5'-mono-phosphate dehydrogenase; hepatomas;	
KW	guanosine monophosphate; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	42..1584
FT		/*tag= a
FT	polyA-signal	/product=Human IMPDH
FT		/*tag= b
FT	GC-signal	1..6
FT		/*tag= c
FT		/label=Box 1
FT	GC-signal	19..26
FT		/*tag= d
FT		/label=Box 2
PN	W09001545-A.	
XX		
PD	22-FEB-1990.	
XX		

PF 02-AUG-1989; 89WO-0000344.
XX
PR 12-AUG-1988; 88US-0232302.
XX
PA (ARCH-) ARCH. DEV. CORP.
XX
PI Collart FR, Huberman E;
XX
DR WPI; 1990-083504/11.
DR P-PSDB; AAR05432.
XX
PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
PT used to detect high levels of enzyme activity of tumour cells,
PT esp. hepatomas, and to produce guanosine monophosphate.
XX
PS Claim 8; Fig 1; 51pp; English.
XX
CC The sequence can be used to quantitatively detect IMPDH encoding
CC DNA or RNA by hybridisation, eg in normal and malignant cells,
CC esp. hepatomas.
CC See also AA003541.
XX
SQ Sequence 1642 BP; 411 A; 416 C; 449 G; 366 T; 0 other;

Query Match 98.9%; Score 1635.6; DB 11; Length 1642;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GGGCGTCTCGGAGACACGCGCGTGTCTGTGTGGCCATGGCCGACTACCTGATTGA 66
Db 1 GGGCGTCTCGGAGACACGCGCGTGTCTGTGTGGCCATGGCCGACTACCTGATTGA 60
QY 67 GTGGGGGACGTCCTACGTGCCACAGACGGACTCACAGACACAGCTCTTCAACTGCG 126
Db 61 GTGGGGGACGTCCTACGTGCCACAGACGGACTCACAGACACAGCTCTTCAACTGCG 120
QY 127 GAGACGCTCACCTACATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCAGTCAG 186
Db 121 GAGACGCTCACCTACATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCAGTCAG 180
QY 187 ACCAGGTGACCTGACTTCTGCTTGACCAAGAAAATCACTTTAAGACCCCACTGGTTT 246
Db 181 ACCAGGTGACCTGACTTCTGCTTGACCAAGAAAATCACTTTAAGACCCCACTGGTTT 240
QY 247 CCTCTCCATGGACACAGTCACAGAGCTGGGATGGCCATAGCAATGGCGTTACAGGCG 306
Db 241 CCTCTCCATGGACACAGTCACAGAGCTGGGATGGCCATAGCAATGGCGTTACAGGCG 300
QY 307 GTATTGCTTCATCCACCAACTGTACACCTGAATTCACGCCAATGAAGTTCGGAAG 366
Db 301 GTATTGCTTCATCCACCAACTGTACACCTGAATTCACGCCAATGAAGTTCGGAAG 360
QY 367 TGAAGAAATATGAACAGGAGTTCATCAGACCCTGTGTCTCAGCCCCAAGATCGCG 426
Db 361 TGAAGAAATATGAACAGGAGTTCATCAGACCCTGTGTCTCAGCCCCAAGATCGCG 420
QY 427 TCGCGGATGTTTTTGAGGCCAAGCGCCGCGATGGTTTCTGCGGTATCCCAATCACAGACA 486
Db 421 TCGCGGATGTTTTTGAGGCCAAGCGCCGCGATGGTTTCTGCGGTATCCCAATCACAGACA 480
QY 487 CAGGCGGATGGGAGCGGCTTGTGGGCATCATCTCTCCAGGGACATTTGATTTTCTCA 546
Db 481 CAGGCGGATGGGAGCGGCTTGTGGGCATCATCTCTCCAGGGACATTTGATTTTCTCA 540
QY 547 AAGAGAGAAACATGACTGTTTCTTGAAGAGATTAATGACAAGAGGAAAGACTTGTGG 606
Db 541 AAGAGAGAAACATGACTGTTTCTTGAAGAGATTAATGACAAGAGGAAAGACTTGTGG 600
QY 607 TAGCCCCCGCAGCATCACACTGAAGAGGCAATGAATTTTCAGCGCAGACAAGAAG 666
Db 601 TAGCCCCCGCAGCATCACACTGAAGAGGCAATGAATTTTCAGCGCAGACAAGAAG 660
QY 667 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGACC 726

Db 661 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCCATCATTTGCCCGGACAGACC 720
QY 727 TGAAGAGAATCGGACTACCCACTAGCCTCCAAGATGCCAAGAAACAGACTGTGTGTG 786
Db 721 TGAAGAGAATCGGACTACCCACTAGCCTCCAAGATGCCAAGAAACAGACTGTGTGTG 780
QY 787 GGGCAGCCATTGGCACTCATGAGATGACAAAGTATAGGCTGGACTTGTCTCGCCAGGCTG 846
Db 781 GGGCAGCCATTGGCACTCATGAGATGACAAAGTATAGGCTGGACTTGTCTCGCCAGGCTG 840
QY 847 GTGTGATGTAGTGTGTTTTGGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGA 906
Db 841 GTGTGATGTAGTGTGTTTTGGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGA 900
QY 907 TCAAGTACATCAAAAGACAATACCCTAATCTCCAAGTCAATTGGAGGCAATGTGTCACTG 966
Db 901 TCAAGTACATCAAAAGACAATACCCTAATCTCCAAGTCAATTGGAGGCAATGTGTCACTG 960
QY 967 CTGCCAGGCCCAAGAACCTCAATTGATGCAGGTGTGATGCCCTGCGGGTGCGCATGGGAA 1026
Db 961 CTGCCAGGCCCAAGAACCTCAATTGATGCAGGTGTGATGCCCTGCGGGTGCGCATGGGAA 1020
QY 1027 GTGCTCCATCTGCATTTATCCAGAGAGTGTGCGCTGTGGCGGGCCCCCAAGCAACAGCAG 1086
Db 1021 GTGCTCCATCTGCATTTACGCAAGAGTGTGCGCTGTGGCGGGCCCCCAAGCAACAGCAG 1080
QY 1087 TGTACAAGGTGTATGAGTATGCACGGCGCTTTGGTGTTCGGTCAATTGCTGATGGAGAA 1146
Db 1081 TGTACAAGGTGTACAGATATGCACGGCGCTTTGGTGTTCGGTCAATTGCTGATGGAGAA 1140
QY 1147 TCCAAAATGTGGTCAATATTGCGAAAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGG 1206
Db 1141 TCCAAAATGTGGTCAATATTGCGAAAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGG 1200
QY 1207 GCTCTCTCTGGCTGCCACCACTGAGGCCCTGTGTGAATACTCTTTTCCGATGGGATCC 1266
Db 1201 GCTCTCTCTGGCTGCCACCACTGAGGCCCTGTGTGAATACTCTTTTCCGATGGGATCC 1260
QY 1267 GGCTTAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCAACCTCAGAGCC 1326
Db 1261 GGCTTAAGAAATATCGCGGTATGGGTTCTCTCGATGCCATGGACAAGCAACCTCAGAGCC 1320
QY 1327 AGAACAGATATTTCAGTGAAGCTGACAAAATCAAAAGTGCGCCAGGGAGTGTCTGTGCTG 1386
Db 1321 AGAACAGATATTTCAGTGAAGCTGACAAAATCAAAAGTGCGCCAGGGAGTGTCTGTGCTG 1380
QY 1387 TGCAGACAAGAGGTCAATCCACAATTTTGTCCCTTACCTGATTTGCTGGCATCCAACACT 1446
Db 1381 TGCAGACAAGAGGTCAATCCACAATTTTGTCCCTTACCTGATTTGCTGGCATCCAACACT 1440
QY 1447 CATGCCAGGACATTTGGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTTGGGG 1506
Db 1441 CATGCCAGGACATTTGGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTTGGGG 1500
QY 1507 AGCTTAAGTTTGAGAAGAGACGTCTCAGCCCAAGGTGGAAGGTGGCGTCCATAGCCTCC 1566
Db 1501 AGCTTAAGTTTGAGAAGAGACGTCTCAGCCCAAGGTGGAAGGTGGCGTCCATAGCCTCC 1560
QY 1567 ATTGCTATGAGAAGCGGCTTTCTGA AAAAGGATCCAGCACACCTCGGTTTTTTTTT 1626
Db 1561 ATTGCTATGAGAAGCGGCTTTCTGA AAAAGGATCCAGCACACCTCGGTTTTTTTTT 1620
QY 1627 CAATTAAGTTTGAAGAGACC 1648
Db 1621 CAATTAAGTTTGAAGAGACC 1642

RESULT 2
ABV29489
ID ABV29489 standard; cDNA; 2277 BP.
XX
AC ABV29489;

|||||
Db 1411 AGACACATATTTTCAGTGAAGCTGACAAAAATCAAAAGTGGCCAGGAGTGTCTGTGCTG 1470
QY 1387 TGCAGGACAAAGGTCATCCACAATTGTCCCTTACCTGATTTGCTGGCATCCAACT 1446
Db 1471 TGCAGGACAAAGGTCATCCACAATTGTCCCTTACCTGATTTGCTGGCATCCAACT 1530
QY 1447 CATGCCAGGACATTTGTGCCAAGAGCTTGACCCAGTCCGAGCCATGATGTACTCTGGG 1506
Db 1531 CATGCCAGGACATTTGTGCCAAGAGCTTGACCCAGTCCGAGCCATGATGTACTCTGGG 1590
QY 1507 AGCTTAAAGTTTGAGAAGAGACGTCCTCAGCCAGGTGGAAGGTGGCGTCCATAGCCTCC 1566
Db 1591 AGCTTAAAGTTTGAGAAGAGACGTCCTCAGCCAGGTGGAAGGTGGCGTCCATAGCCTCC 1650
QY 1567 ATTCGTATGAGAAGCGGCTTTCTGAAAAGGAGATCCAGCACCTCTCGGTTT TTTT 1626
Db 1651 ATTCGTATGAGAAGCGGCTTTCTGAAAAGGAGATCCAGCACCTCTCGGTTT TTTT 1710
QY 1627 CAATAAAGTTTAGAAGA 1645
Db 1711 CAATAAAGTTTAGAAGA 1729

RESULT 3
ABV23631
ID ABV23631 standard; cDNA; 1677 BP.
XX
AC ABV23631;
XX 16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 23622.
DE Human prostate expression marker cDNA 23622.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 4329; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 1677 BP; 428 A; 446 C; 445 G; 358 T; 0 other;
Query Match 89.2%; Score 1475; DB 23; Length 1677;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1568; Conservative 0; Mismatches 15; Indels 44; Gaps 4;
QY 15 CTGGAGACACGCGCGGTGCTCTGTGTTGCCATGGCCGACTACCTGATTAGTGGGGC 74
Db 1 CTGGAGACACGCGCGGTGCTCTGTGTTGCCATGGCCGACTACCTGATTAGTGGGGC 60
QY 75 ACGTCTACGTGCGCAGACGAGGACTCAGACAGCAGCTCTCAACTGCGGAGAGCGC 134
Db 61 ACGTCTACGTGCGCAGACGAGGACTCAGACAGCAGCTCTCAACTGCGGAGAGCGC 120
QY 135 CTCACCTACATGACTTTCTCATTTCTCCCTGGGTACATGCACTTCACTGCAGACGAGTG 194
Db 121 CTCACCTACAA-----ACCAAGTG 139
QY 195 GACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGTTCTCTCCC 254
Db 140 GACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGTTCTCTCCC 199
QY 255 ATGGACACAGTCACAGAGGCTGGGATGGCCATAGCAATGCGCGCTTACAGCGGTATTGGC 314
Db 200 ATGGACACAGTCACAGAGGCTGGGATGGCCATAGCAATGCGCGCTTACAGCGGTATTGGC 259
QY 315 TTCATCCACCACAACCTGTACACCTGAATTCAGGCGCCATGAAGTTCGGAAGTGAAGAA 374
Db 260 TTCATCCACCACAACCTGTACACCTGAATTCAGGCGCCATGAAGTTCGGAAGTGAAGAA 319
QY 375 TATGAACAGGATTCATACAGACCCTGTGTCCTCAGGCCCAAGGATCGCGTGGGAT 434
Db 320 TATGAACAGGATTCATACAGACCCTGTGTCCTCAGGCCCAAGGATCGCGTGGGAT 379
QY 435 GTTTTGAAGCCCAAGGCCGCGCATGTTTCTGCGGTATCCCAATCACAGACAGCGCGG 494
Db 380 GTTTTGAAGCCCAAGGCCGCGCATGTTTCTGCGGTATCCCAATCACAGACAGCGCGG 439
QY 495 ATGGGAGCGCGCTTGGTGGGATCATCTCTCCAGGACATTTTCTCAAGAAGAG 554
Db 440 ATGGGAGCGCGCTTGGTGGGATCATCTCTCCAGGACATTTTCTCAAGAAGAG 499
QY 555 GAACATGACTGTTCTTGGAGAGATTAATGACAAAGAGGAGAACTTGGTGTAGCCCC 614
Db 500 GAACATGACTGTTCTTGGAGAGATTAATGACAAAGAGGAGAACTTGGTGTAGCCCC 559
QY 615 CGACATCACACTGAAGGAGGCAATGAATTTCTGACGCGCAGCAAGAGGAAAGTTG 674
Db 560 GCAGCATCACACTGAAGGAGGCAATGAATTTCTGACGCGCAGCAAGAGGAAAGTTG 619
QY 675 CCCATTGTAATGAAGATGATGAGCTTGTGGCCATTCATGCCCCGACAGACTGAAGAG 734
Db 620 CCCATTGTAATGAAGATGATGAGCTTGTGGCCATTCATGCCCCGACAGACTGAAGAG 679
QY 735 AATCGGACTACCCACTAGCTTCCAAAGATGCCAAGAAACAGCTGCTGTGTGGGAGCC 794
Db 680 AATCGGACTACCCACTAGCTTCCAAAGATGCCAAGAAACAGCTGCTGTGTGGGAGCC 739
QY 795 ATGGCACTCATGAGATGACAGATATAGGCTGAGCTTGTGCCCCAGGCTGGTGTGAT 854
Db 740 ATGGCACTCATGAGATGACAGATATAGGCTGAGCTTGTGCCCCAGGCTGGTGTGAT 799
QY 855 GTAGTGTTTGGACTCTTCCAGGGAATTCATCTTCAGATCAATATGATCAAGTAC 914
Db 800 GTAGTGTTTGGACTCTTCCAGGGAATTCATCTTCAGATCAATATGATCAAGTAC 859

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QY 915 ATCAAGACAATACCCCTAATCTCCAGTCAATTGGAGGCAATGTGGTCACTGCTGCCAG 974
Db 860 ATCAAGACAATATACCTAATCTCCAAGTCAATTGGAGGCAATGTGGTCACTGCTGCCAG 919
QY 975 GCCAAGAACCTCATTTGATGCAGTGTGATGCCCTGCGGCTGGGCATGCGAAGTGGCTCC 1034
Db 920 GCCAAGAACCTCATTTGATGCAGTGTGATGCCCTGCGGCTGGGCATGCGAAGTGGCTCC 979
QY 1035 ATCTGCATTATCCAGGAAGTGTGCTGCTGTGGCGGCCCAAGCAACAACAGTGTACAAG 1094
Db 980 ATCTGCATTATCCAGGAAGTGTGCTGCTGTGGCGGCCCAAGCAACAACAGTGTACAAG 1039
QY 1095 GTGTATGAGTATGCACGGCCTTGTGTCCGGTCAATTGCTGATGGAAGATCCAAAAT 1154
Db 1040 GTGTACAGATATGCACGGCCTTGTGTCCGGTCAATTGCTGATGGAAGATCCAAAAT 1099
QY 1155 GTGGCTCATATTGCGAAAGCCTTGCCCTTGGGGCCTCCACAGTCATGATGGCTCTCTC 1214
Db 1100 GTGGCTCATATTGCGAAAGCCTTGCCCTTGGGGCCTCCACAGTCATGATGGCTCTCTC 1159
QY 1215 CTGGCTGCCACCACTGAGGCCCTGTGATACTTCTTTCCGATGGGATCCGGCTAAG 1274
Db 1160 CTGGCTGCCACCACTGAGGCCCTGTGATACTTCTTTCCGATGGGATCCGGCTAAG 1219
QY 1275 AAATATCGCGGTATGGGTCTCTGCAATGCCATGACACAAGCACCTCAGCGCCAGAACA 1334
Db 1220 AAATATCGCGGTATGGGTCTCTGCAATGCCATGACACAAGCACCTCAGCGCCAGAACA 1279
QY 1335 TATTTCAATGAGCTGACAAATCAAGTGGGCCAGGAGTGTCTGCTACTGTGACAGGAC 1394
Db 1280 TATTTCAATGAGCTGACAAATCAAGTGGGCCAGGAGTGTCTGCTACTGTGACAGGAC 1339
QY 1395 AAAGGTCATCCACAATTTGTCCCTTACCTGATTGCTGGCATCCAACTCATGCCAG 1454
Db 1340 AAAGGTCATCCACAATTTGTCCCTTACCTGATTGCTGGCATCCAACTCATGCCAG 1399
QY 1455 GACATTGCTGCCAAGAGCTTGACCCCAAGTCCGAGCATGATGTAAGTGGAGCTTAAG 1514
Db 1400 GACATTGCTGCCAAGAGCTTGACCCCAAGTCCGAGCATGATGTAAGTGGAGCTTAAG 1459
QY 1515 TTTGAGAAGAGAAGCTCTCAGCCCAAGTGGAAAGTGGCGTCCA-TAGCTCATTCGTA 1573
Db 1460 TTTGAGAAGAGAAGCTCTCAGCCCAAGTGGAAAGTGGCGTCCA-TAGCTCATTCGTA 1519
QY 1574 T-GAGAAGCGGCTTTTCTGAAGAGGATCCAGCAC-ACCTCCTCGGTTT TTTTTCATA 1631
Db 1520 TGGAGAAGCGGCTTTCTGAAGAGGATCCAGCACACCTCCTCGGTT TTTTTCACTA 1579
QY 1632 AAAGTTT 1638
Db 1580 ACACGTT 1586
```

```
RESULT 4
ABV24746
ID ABV24746 standard; cDNA; 1677 BP.
XX AC ABV24746;
XX XX 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 24737.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharm codyanamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
```

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XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE,
PI WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX Claim 1; Page 4726; 11750pp; English.
PS The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 1677 BP; 428 A; 446 C; 445 G; 358 T; 0 other;
SQ
Query Match 89.2%; Score 1475; DB 23; Length 1677;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1568; Conservative 0; Mismatches 15; Indels 44; Gaps 4;
QY 15 CTGGAGACAC3CGGCGGTGTCTCTGTGTGGCCATGCGCCGACTACCTGATTAGTGGGCG 74
Db 1 CTGGAGACAC3CGGCGGTGTCTCTGTGTGGCCATGCGCCGACTACCTGATTAGTGGGCG 60
QY 75 ACGTCTACGCTGCCAGACGACGACTCACAGCAGCAGCAGCTCTTCAACTGCGGAGACGGC 134
Db 61 ACGTCTACGCTGCCAGACGACGACTCACAGCAGCAGCAGCTCTTCAACTGCGGAGACGGC 120
QY 135 CTACCTACATGACTTTCTCTATTTCTCCCTGGGTACATGCACTTCACTGACAGCAGGTG 194
Db 121 CTACCTACAA-----ACCAAGTG 139
QY 195 GACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTTCTCTGCC 254
Db 140 GACCTGACTTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTTCTCTGCC 199
QY 255 ATGACACAGTTCACAGAGGCTGGATGGCCATAGCAATGCGCCTTACAGGCGGTATGGC 314
Db 200 ATGACACAGTTCACAGAGGCTGGATGGCCATAGCAATGCGCCTTACAGGCGGTATGGC 259
QY 315 TTTCATCCACCAACTGTACACCTGAATTCAGGCCCAATGAAGTTCGGAAGTGAAGAAA 374
Db 260 TTTCATCCACCAACTGTACACCTGAATTCAGGCCCAATGAAGTTCGGAAGTGAAGAAA 319
QY 375 TATGACAGGGATTCATCACAGACCCCTGTGCTCAGCCCCAAGGATCGGTGCGGAT 434
Db 320 TATGACAGGGATTCATCACAGACCCCTGTGCTCAGCCCCAAGGATCGGTGCGGAT 379
QY 435 GTTTTGGAGGCCAAGGCCGCGATGGTTTCTGCGGTATCCCAATCACAGACACAGCCGG 494
Db 380 GTTTTGGAGGCCAAGGCCGCGCGATGGTTTCTGCGGTATCCCAATCACAGACACAGCCGG 439
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QY 187 ACCAGTGGACCTGACTTCTGCTGTGACCAAGAAATCCTCTTAAAGACCCCACTGTTT 246
Db 499 ACCAGTGGACCTGACTTCTGCTGTGACCAAGAAATCCTCTTAAAGACCCCACTGTTT 558
QY 247 CCTCTCCATGGACACAGTACACAGAGCTGGGATGGCCATAGCAATGCGCTTACAGGCG 306
Db 559 CCTCTCCATGGACACAGTACACAGAGCTGGGATGGCCATAGCAATGCGCTTACAGGCG 618
QY 307 GTATTGGCTTCATCCACCACAACCTGACCTGAATTCCAGGCCAATAAGTTCCGAAAG 366
Db 619 ----- 618
QY 367 TGAAGAAATATGAACAGGATTCATCAGACCCCTGTGCTCTCAGCCCAAGGATCGCG 426
Db 619 -----ATGATTCATCAGACCCCTGTGCTCTCAGCCCAAGGATCGCG 663
QY 427 TGGGGATGTTTTTTGAGGCCAAGCCCGCATGTTTCTGCGTATCCCAATCAGAGACA 486
Db 664 TGGGGATGTTTTTTGAGGCCAAGCCCGCATGTTTCTGCGTATCCCAATCAGAGACA 723
QY 487 CAGCCCGATGGGAGCCGCTTGGTGGCATCATCTCCTCCAGGGACAATTGATTTTCTCA 546
Db 724 CAGCCCGATGGGAGCCGCTTGGTGGCATCATCTCCTCCAGGGACAATTGATTTTCTCA 783
QY 547 AAGAGAGAAACATGACTGTTTCTTGAAGAGATATGACAAAGAGGGAGAGCTTGTGTG 606
Db 784 AAGAGAGAAACATGACTGTTTCTTGAAGAGATATGACAAAGAGGGAGAGCTTGTGTG 843
QY 607 TAGCCCCCGCAGCATCACACTGAAGGAGGCAAAATGAATTTCTGACGCCAGCAAGAGG 666
Db 844 TAGCCCCCGCAGGCATCACACTGAAGGAGGCAAAATGAATTTCTGACGCCA-CAAGAGG 902
QY 667 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCATCATGCGGACAGAGCC 726
Db 903 GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTGTGGCATCATGCGGACAGAGCC 962
QY 727 TGAAGAGAAATCGGAGCTACCCACTAGCCTCCAAAGATGCCAAGAAAGCTGTGTGTG 786
Db 963 TGAAGAGAAATCGGAGCTACCCACTAGCCTCCAAAGATGCCAAGAAAGCTGTGTGTG 1022
QY 787 GGGCAGCCATTGGCACTCATGAGGATGACAAGTATAGCTGAGCTGCGCCAGGCTG 846
Db 1023 GGGCAGCCATTGGCACTCATGAGGATGACAAGTATAGCTGAGCTGCGCCAGGCTG 1082
QY 847 GTGTGATGTAGTGTGTTTGGACCTTCCAGGGAATTTCCATCTCCGATCAATATGA 906
Db 1083 GTGTGATGTAGTGTGTTTGGACCTTCCAGGGAATTTCCATCTCCGATCAATATGA 1142
QY 907 TCAAGTACATCAAGACAATAACCTAATCTCCAGATCATTTGAGGCAATGTGTCACTG 966
Db 1143 TCAAGTACATCAAGACAATAACCTAATCTCCAGATCATTTGAGGCAATGTGTCACTG 1202
QY 967 CTGCCAGGCCAAGAACCTCATTTGATGCAAGTGTGATGCCCTGCGGGGGGCATGGAA 1026
Db 1203 CTGCCAGGCCAAGAACCTCATTTGATGCAAGTGTGATGCCCTGCGGGGGGCATGGAA 1262
QY 1027 GTGGCTCCATCTGCATATATCCAGAGAGTGTGCGCTGTGGCGGCGCCAGCAACAGCAG 1086
Db 1263 GTGGCTCCATCTGCATATATCCAGAGAGTGTGCGCTGTGGCGGCGCCAGCAACAGCAG 1322
QY 1087 TGTACAAGGTGTATGAGTATGCACGGCGCTTGTGTCTCCGGTCAATGTGATGAGGAA 1146
Db 1323 TGTACAAGGTGTATGAGTATGCACGGCGCTTGTGTCTCCGGTCAATGTGATGAGGAA 1382
QY 1147 TCCAAATGTGGGTCAATATGCGGAAGCCTTGGCCCTTGGGCGCTCCAGAGTCATGATGG 1206
Db 1383 TCCAAATGTGGGTCAATATGCGGAAGCCTTGGCCCTTGGGCGCTCCAGAGTCATGATGG 1442
QY 1207 GCTCTCTCTGGCTGCCACCACTGAGCCCCCTGGTGAATACTTCTTTCCGATGGATCC 1266
Db 1443 GCTCTCTCTGGCTGCCACCACTGAGCCCCCTGGTGAATACTTCTTTCCGATGGATCC 1502

QY 1267 GGCTAAGAAATATCGCGGATATGGGTTCTCTCGATGCCATGACACACCTCAGACGCC 1326
Db 1503 GGCTAAGAAATATCGCGGATATGGGTTCTCTCGATGCCATGACACACCTCAGACGCC 1562
QY 1327 AGACAGATATTTTCAGTGAAGCTGACAAATCAAAAGTGCGCCAGGGAGTGTCTGTGCTG 1386
Db 1563 AGACAGATATTTTCAGTGAAGCTGACAAATCAAAAGTGCGCCAGGGAGTGTCTGTGCTG 1622
QY 1387 TGCAGGACAAAGGGTCAATCCACAAATTTGTCCTTACCTGATTGCTGGCATCCAACT 1446
Db 1623 TGCAGGACAAAGGGTCAATCCACAAATTTGTCCTTACCTGATTGCTGGCATCCAACT 1682
QY 1447 CATGCCAGGACATTTGTTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTTGGGG 1506
Db 1683 CATGCCAGGACATTTGTTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTTGGGG 1742
QY 1507 AGCTTAAGTTTGAGAAGAGAACGTCCTCAGCCCAAGTGGGAAGTGGCGTCCATAGCCTCC 1566
Db 1743 AGCTTAAGTTTGAGAAGAGAACGTCCTCAGCCCAAGTGGGAAGTGGCGTCCATAGCCTCC 1802
QY 1567 ATTCGTATGACAAAGCGGCTTTCTGAAAAAGGATCCAGACACCTCCTCGGTTTTTTT 1626
Db 1803 ATTCGTATGACAAAGCGGCTTTCTGAAAAAGGATCCAGACACCTCCTCGGTTTTTTT 1862
QY 1627 CAATAAAGTTTAGAAAGA 1645
Db 1863 CAATAAAGTTTAGAAAGA 1881

RESULT 6
AA003541
ID AA003541 standard; DNA: 1620 BP.
XX
AC AA003541;
XX
DT 31-AUG-1990 (first entry)
XX
DE Chinese hamster IMPDH.
XX
KW Inosine 5'-mono-phosphate dehydrogenase; hepatomas;
KW guanosine monophosphate; ss.
XX
OS *Cricetulus* sp.
PN W09001545-A.
XX
PD 22-FEB-1990.
XX
PF 02-AUG-1989; 89WO-0000344.
XX
PR 12-AUG-1988; 88US-0232302.
XX
PA (ARCH-) ARCH. DEV. CORP.
XX
PI Collart FR, Huberman E;
XX
DR WPI: 1990-083504/11.
DR N-PSDB: AA003541.

PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
PT used to detect high levels of enzyme activity of tumour cells,
PT esp. hepatomas, and to produce guanosine monophosphate.
XX
PS Claim 8; Fig 2; 51pp; English.
XX
CC The sequence can be used to quantitatively detect IMPDH encoding
CC DNA or RNA by hybridisation, eg in normal and malignant cells,
CC esp. hepatomas.
CC See also AA003540.
XX
SQ Sequence 1620 BP; 423 A; 369 C; 421 G; 406 T; 1 other;

Query Match 79.8%; Score 1320.2; DB 11; Length 1620;

Best Local Similarity 88.8%; Pred. No. 0;		Matches 1441; Conservative 0; Mismatches 178; Indels 4; Gaps 1;	
QY	23	CACGGCGGCTGTCTGTGTGGCCATGGCCGACTACCTGATTAAGTGGGGCAGCTCTTA	82
Db	1	CACGGCTCCGTGCTCCTGTTGGCCATGGCGGACTACCTGATTAAGCGAGGCACATCTTA	60
QY	63	CGTGCAGACGACGGACTCACAGCACAGCAGCTCTTCACTGGCGAGAGCGGCTCACCTA	142
Db	61	CGTGCAGACGACGGGCTCACAGCGCAGCAGCTCTTCACTGGCGGAGTGGCTCACCTA	120
QY	143	CAATGACTTTCTCATTTCTCCCTGGGTACATCGACTTCACTGACAGACCAAGTGGACCTGAC	202
Db	121	CAACGATTTTCTCATTTCTTCCGTATATCGACTTCACTGCCGACCAAGTGGATTTGAC	180
QY	203	TTCTGCTCTGACCAAGAAATCACTCTTAAGACCCCACTGGTTCTCTCCATGGACAC	262
Db	181	CTCTGCTCTAAGAAAGATCACCTGAAGACCCCACTGGTTCTCTCACCTATGACAC	240
QY	263	AGTCAAGAGCGCTGGATGGCCATAGCAATGGCGCTTACAGCGGTAATGGCTTCATCCA	322
Db	241	TGTCACAGAGCGTGAATGGCCATGCAATGGCGCTTACAGAGGTAATGGCTTCATCCA	300
QY	323	CCACAACTGTACACCTGAATTCAGGCCCAATGAAGTTCGAAAGTGAAGAAATATGAACA	382
Db	301	CCACAACTGTACACCTGAATTCAGGCCCAATGAAGTTCGAAAGTGAAGAAATATGAACA	360
QY	383	GGGATTCATCACAGACCCCTGTGCTCTCAAGCCCAAGGATCGGCTGGGGATGTTTGA	442
Db	361	GGGATTCATTAACCTGATCCTGTAGVCCCTTAAGCCCAAGGATCGTGTAGGGATGTTTGA	420
QY	443	GGCCAGGCGCGGCTGTTCTGCGGTATCCCAATCACAGACAGCGCGGATGGGAG	502
Db	421	AGCCAAAGCCAGGCTGCTCTGTGTATCCCATCACAGATACAGGCGGATGGGAG	480
QY	503	CCGCTGTGGGCTCATCTCTCCAGGAGCATTTGTTCTCAAGAGGAGGAGCAACATGA	562
Db	481	TCGACTGTGGGCTCATTTCTTCAAGGATATTGATTTTCTCAAGAGGAGGAGCATGA	540
QY	563	CTGTTTCTTGAAGAGATTAATGACAAAGGGAAGACTTGTGTAGCCCCCGGACGAT	622
Db	541	CCGTTTCTTGAAGAGATCATGACAAAGGGAAGATTGTGTGGCCCCCTGCAGCAT	600
QY	623	CACACTGAAGGAGCAAAATGAAATTTCTCAGCGCAGCAGCAAGAGGAAAGTTGCCATTGT	682
Db	601	CACCTGAAGGAGCAAAATGAAATTTCTCAGCGCAGCAGTAAGGAAAGGAAAGTTGCCATTGT	660
QY	683	AAATGAAGATGATGAGCTTGTGGCCATTTGCCCGGACAGACCTGAAGAAGATCGGA	742
Db	661	GAATGAAGATGATGAGCTGTGAGCCATTTGCTCGGACAGACCTGAAGAAGATCGTGA	720
QY	743	CTACCCACTAGCCTCCAAAGATGCCAAGAACAGCTGCTGTGTGGGCAACCATTTGGCAC	802
Db	721	TTACCCATTGGCTTCCAAAGATGCCAAGAACAGCTTACTATGTGGGCAACCATTTGGTAC	780
QY	803	TCATGAGGATGACAGATATAGGCTGGACTTGTCTGCCAGGCTGGTGTGATGTAGTGT	862
Db	781	TCATGAGGATGACAGATATAGGCTGGACTTGTCTGTGCTGTGTGATGTAGTGT	840
QY	863	TTTGACTCTTCCAGGAAATTCATCTTCCAGATCAATATATGATCAAGTACATCAAGA	922
Db	841	TTTGACTCTTCCAGGAAATTCATCTTCCAAATCAATATATGATCAATATCAAGA	900
QY	923	CAATACCCCTAATCTCCAAGTATTTGAGGCAATGTGCTCACTGCTGCCAGGCCAAGAA	982
Db	901	GAATATACCCCAATCTCCAAGTATTTGAGGCAATGTAGTCACTGCTCAAGCCAAGAA	960
QY	983	CCTCATTGATGAGGATGTGGATGCCCTCGCGGTGGGCATGGGAAGTGGCTTCATCTGCAT	1042
Db	961	CCTCATAGACGAGGTGTGATGCTCTGCGAGTTGGCATGGGCTGTGCTTCATCTGCAT	1020
QY	1043	TATCCAGGAAGTGTGGCTGTGGGCGGCCCAAGCAACAGCAGTGTACAGGTGTATGA	1102

Db	1021	TACTCAGGAAGTGTGGCTGTGTGGTCGGCCCCCAAGCAACAGCAGTGTACAAAGTTTCTGA	1080
QY	1103	GTAAGCAGCGCGCTTTGGTTCCGGTCAATTTGCTGATGAGGAATCCAAATGTGGCTCA	1162
Db	1081	GTAAGCTCGCGCTTTGGTGTCTCTGTTATTTGCTGATGAGGAATCCAAATGTGGCTCA	1140
QY	1163	TATTGCGAAAGCCTTGGCCCTTGGGGCTCCACAGTCAATGATGGGCTCTCTCGGCTGC	1222
Db	1141	TATTGCCAAAGCTTTGGCTCTTGGAGCTTCTACAGTCAATGATGGGCTCCCTCTGGCTGC	1200
QY	1223	CACCACTGAGGCCCCCTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAGAAATATCG	1282
Db	1201	CACCACTGAGGCCCCCTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAGAAATATCG	1260
QY	1283	CGTTATGGGTTCTCTGATGCCATGGACAAGCACCCTCAGCAGCCAGAACAGATATTGAG	1342
Db	1261	TGTTATGGGTTCTCTGATGCCATGGACAAGCATCTCAGCAGCCAGAACGATATTGAG	1320
QY	1343	TGAAGCTGACAAATCAAAAGTGGCCCAAGGAGTGTCTGCTGTGCAGGACAAAGGCTC	1402
Db	1321	TGAAGCTGACAAATCAAAAGTGGCCCAAGGAGTGTCTGCTGTGCAGGACAAAGGCTC	1380
QY	1403	AATCCAAATTTGTCCCTTACCTGATTTGCTGGCATCCAACTCATGCCAGACATTTGG	1462
Db	1381	TATCCAAAGTTGCTCCCTTATTTGATTTGCTGGCATCCAGCATTCCTGTACAGACATTTG	1440
QY	1463	TGCCAAGACCTTGACCCCAAGTCCAGCCCATGATGTACTCTGGGGAAGCTTAAGTTGAGA	1522
Db	1441	TGCCAAGAGTTTAACCCCAAGTCCAGCCCATGATGTACTCTGGGGAAGCTTAAGTTGAGA	1500
QY	1523	GAGAAGCTCCTCAGCCAGGTGGAAGTGGCGTCCATAGCCTCCATTGCTATGAGAAGCG	1582
Db	1501	GAGAAGCTCCTCAGCTCAGGTGGAAGTGGTCCACAGCCTTCATTGCTATGAGAAGCG	1560
QY	1583	GCTTTTCTGAAGGAGTCCAGCACACCTCTCGGTTTTTTTCAATAAAGTTAGAA	1642
Db	1561	GCTTTTCTGAAGGAGTCCAGCTCAGTA---TATGCTTGAATTTTCAATAAAGTTTGA	1616
QY	1643	AGA 1645	
Db	1617	AAA 1619	
RESULT 7			
AAF21634			
ID	AAF21634 standard; DNA; 2019 BP.		
XX	AAF21634;		
AC			
XX			
DT	27-MAR-2001 (first entry)		
XX			
DE	Human breast and ovarian cancer associated antigen gene SEQ ID 21.		
XX			
KW	Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;		
KW	neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;		
KW	antidiabetic; antineoplastic; antitumor; antitumor; antitumor;		
KW	antibacterial; antifungal; antiparasitic; cardiac; immune disorder;		
KW	Addison's disease; allergy; autoimmune haemolytic anaemia;		
KW	autoimmune thyroiditis; diabetes mellitus; Crohn's disease;		
KW	multiple sclerosis; rheumatoid arthritis; ulcerative colitis;		
KW	cardiovascular disorder; wound healing; neurological disease; ds.		
OS	Homo sapiens.		
XX			
PN	WO20005173-A1.		
XX			
PD	21-SEP-2000.		
XX			
PF	08-MAR-2000; 2000WO-US05881.		
XX			
PR	12-MAR-1999; 99US-0124270.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		

XX Rosen CA, Ruben SM;
PI
XX WPI; 2000-611515/58.
DR P-PSDB; AAB58731.
DR
XX
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
XX
XX
PS Claim 1; Page 496; 1299pp; English.

CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antiinflammatory; antilulcer; vulnerary; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiant activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and agonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemias; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 2019 BP; 512 A; 483 C; 538 G; 476 T; 10 other;

Query Match 74.8%; Score 1236.8; DB 21; Length 2019;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1263; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

QY 370 AGAATATGTAACAGGATTCATCACAGCCCTGTGTCCTCAGCCCCAGGATCGCGTGC 429
DB 697 AGAATATGTAACAGGATTCATCACAGCCCTGTGTCCTCAGCCCCAGGATCGCGTGC 756
QY 430 GGGATGTTTTGAGGCCAAGGCCCGGCATGTTCTGCGGTATCCCAATCACAGACACAG 489
DB 757 GGGATGTTTTTRAGGCCAAGGCCCGGCATGTTCTGCGGTATCCCAATCACAGACACAG 816
QY 490 GCCCGATGGGAGCGCGCTTGTTGGGCATCTCTCCAGGCGACATTTATTCTCAAG 549
DB 817 GCCCGATGGGAGCGCGCTTGTTGGGCATCTCTCCAGGCGACATTTATTCTCAAG 876
QY 550 AGGAGACATGACTGTTCTTGGAGAGATATGACAAAGAGGGAGACTTGTGTAG 609
DB 877 AGGAGACATGACTGTTCTTGGAGAGATATGACAAAGAGGGAGACTTGTGTAG 936
QY 610 CCCCCCGACATCACACTGAAGGAGCAATGAATTTCTGACGGCAACAAGAGGAA 669
DB 937 CCCCCCGACATCACACTGAAGGAGCAATGAATTTCTGACGGCAACAAGAGGAA 995
QY 670 AGTTGCCCATTTGAATGAAGATGATGAGCTTGTGGCATCATTTGCCGACAGCCTGA 729
DB 996 AGTTGCCCATTTGAATGAAGATGATGAGCTTGTGGCATCATTTGCCGACAGCCTGA 1055
QY 730 AGAAGATCGGAGCTACCCACTAGCCTCCAAAGATGCCAAGAAGAGAGTGTGTGGGG 789
DB 1056 AGAAGATCGGAGCTACCCACTAGCCTCCAAAGATGCCAAGAAGAGAGTGTGTGGGG 1115
QY 790 CAGCCATTCGCACTCATGAGATGACACATATAGGCTGGACTTGCTGCCAGGCTGGTG 849
DB 1116 CAGCCATTCGCACTCATGAGATGACACATATAGGCTGGACTTGCTGCCAGGCTGGTG 1175
QY 850 TGGATGTAGTGTGTTTGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGATCA 909

DB 1176 TGGATGTAGTGTGTTTGACTCTTCCAGGGAATTCATCTTCCAGATCAATATGATCA 1235
QY 910 AGTACATCAAGACAAATATACCCCTAATCTCCAAGTCAATTTGGAGGCAATGTGTCACCTGCTG 969
DB 1236 AGTACATCAAGACAAATATACCCCTAATCTCCAAGTCAATTTGGAGGCAATGTGTCACCTGCTG 1295
QY 970 CCCAGGCCAAGAACCTCATTTGATGACAGGTGTGGATGCCCTGCCGGTGGGCATGGGAAGTG 1029
DB 1296 CCCAGGCCAAGAACCTCATTTGATGACAGGTGTGGATGCCCTGCCGGTGGGCATGGGAAGTG 1355
QY 1030 GCTCCATCTGACATTTATCCAGGAAGTGTGCGCTGTGGGGGGCCCCAAGCAACAGCAGTGT 1089
DB 1356 GCTCCATCTGACATTTACGCAAGGAAGTGTGCGCTGTGGGGGGCCCCAAGCAACAGCAGTGT 1415
QY 1090 ACAAGGTGTATGAGTATGACAGCGCGCTTTGGTGTTCGGTCAATTTGCTGATGGAGAAATCC 1149
DB 1416 ACAAGGTGTGAGAGTATGACAGCGCGCTTTGGTGTTCGGTCAATTTGCTGATGGAGAAATCC 1475
QY 1150 AAAATGTGGGTCAATATTGCGAAAGCCTTTGGCCCTTGGGGCCCTCCACAGTCATGATGGCT 1209
DB 1476 AAAATGTGGGTCAATATTGCGAAAGCCTTTGGCCCTTGGGGG-CTCCACAGTCATGATGGCT 1534
QY 1210 CTCTCCGTGCGTCCACCACTGACGCGCCCTGTGTAATACTTCTTTCCGATGGATCCGGC 1269
DB 1535 CTCTCCGTGCGTCCACCACTGACGCGCCCTGTGTAATACTTCTTTCCGATGGATCCGGC 1594
QY 1270 TAAAGAAATATCGCGGTATGGGTTCTCTGATGCGCATGGACAAGCAACCTCAGCAGCCAGA 1329
DB 1595 TAAAGAAATATCGCGGTATGGGTTCTCTGATGCGCATGGACAAGCAACCTCAGCAGCCAGA 1654
QY 1330 ACAGATATTTCACTGAAGCTGACAAATCAAAAGTGGCCCAAGGAGTCTGTGTGTGC 1389
DB 1655 ACAGATATTTCACTGAAGCTGACAAATCAAAAGTGGCCCAAGGAGTCTGTGTGTGC 1714
QY 1390 AGGACAAAGGTCAATCCACAATTTGTCCTTACCTGATTTGCTGGCATCCACACTCAT 1449
DB 1715 AGGACAAAGGTCAATCCACAATTTGTCCTTACCTGATTTGCTGGCATCCACACTCAT 1774
QY 1450 GCCAGGACATTTGGTGCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGAGC 1509
DB 1775 GCCAGGACATTTGGTGCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGAGC 1834
QY 1510 TTAAGTTTGAGAAAGAACGTCCTCAGGCCAGGTGGAAGTGGCGTCCATAGCCTCCATT 1569
DB 1835 TTAAGTTTGAGAAAGAACGTCCTCAGGCCAGGTGGAAGTGGCGTCCATAGCCTCCATT 1894
QY 1570 CGTATGAGAAGCGGCTTTCTGAAAAGGGATCCAGCACACCTCCTCGGTTTTTTTCA 1629
DB 1895 CGTATGAGAAGCGGCTTTCTGAAAAGGGATCCAGCACACCTCCTCGGTTTTTTTCA 1954
QY 1630 TAAAGTTTGAAGAAGA 1645
DB 1955 TAAAGTTTGAAGAAGA 1970

RESULT 8
ABK34910
ID ABK34910 standard; cDNA; 1157 BP.
XX
AC ABK34910;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human cDNA encoding secreted protein #48.
XX
KW Human; secreted protein; gene; ss; nutritional supplement; haemophilia;
KW viral infection; bacterial infection; fungal infection; diabetes; asthma;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;
KW autoimmune thyroiditis; allergic reaction; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;
KW coagulation disorder; inflammatory disorder; Crohn's disease; incision;
KW tissue regeneration; wound healing; burn; haematopoiesis;
KW myeloid cell deficiency; lymphoid cell deficiency.

XX Homo sapiens.
OS
XX WO200177288-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 29-MAR-2001; 2001WO-US10224.
PF
XX 06-APR-2000; 2000US-195582P.
PR
XX (GEMY) GENETICS INST INC.
PA
XX Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
PI
XX WPI; 2002-179321/23.
DR
XX
XX Five hundred and ninety two polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for
PT treating immune deficiencies and disorders such as autoimmune disorders
PT
XX
PS Claim 1; Page 93; 372pp; English.
XX
XX The invention relates to 592 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins. The polynucleotides can be used as probes for the
CC identification and isolation of full length cDNA and genomic DNA. The
CC polynucleotides and proteins can also be used as nutritional supplements.
CC The proteins are useful in the treatment of various immune deficiencies
CC and disorders such as viral infections, bacterial infections, fungal
CC infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple
CC sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
CC and conditions (e.g. asthma). They are also useful for treating
CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also
CC useful for tissue regeneration, for wound healing and in the treatment of
CC burns, incisions and ulcers. The proteins are also useful for regulating
CC haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
CC Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
XX
SQ Sequence 1157 BP; 297 A; 270 C; 326 G; 264 T; 0 other;

Query Match 69.0%; Score 1141.6; DB 24; Length 1157;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 489 GGCCGGATGGGAGAGCCGCTTGTTGGGTCATCTCTCCAGGACATTTCTCAAA 548
Db 1 GGCCGGATGGGAGAGCCGCTTGTTGGGTCATCTCTCCAGGACATTTCTCAAA 60
OY 549 GAGGAGACATGACTGTTCTTGAGAGATTAATGACAAAGAGGAGACTTGGTGTA 608
Db 61 GAGGAGACATGACTGTTCTTGAGAGATTAATGACAAAGAGGAGACTTGGTGTA 120
OY 609 GCCCCCCGAGCATCACACTGAAGGAGCAATGAATTTCTGAGCGCAGCAAGAGGA 668
Db 121 GCCCCTGAGGCATCACACTGAAGGAGCAATGAATTTCTGAGCGCAGCAAGAGGA 180
OY 669 AAGTGGCCATTGTAATGAAGATGATGAGCTTGTGGCCATCATGGCCGGACAGACCTG 728
Db 181 AAGTGGCCATTGTAATGAAGATGATGAGCTTGTGGCCATCATGGCCGGACAGACCTG 240
OY 729 AAGAAGAATCGGAGCTACCCACTAGCCTCCAAGATGCCAAGAACAAGCTGCTGTGGG 788
Db 241 AAGAAGAATCGGAGCTACCCACTAGCCTCCAAGATGCCAAGAACAAGCTGCTGTGGG 300
OY 789 GCAGCCATTGGCACTCATGAGATGACAAAGTATAGGCTGGACTTGGCCCCAGGCTGGT 848
Db 301 GCAGCCATTGGCACTCATGAGATGACAAAGTATAGGCTGGACTTGGCCCCAGGCTGGT 360
KW

OY 849 GTGATGTAGTGGTTTGGACTCTTCCCAGGAAATTCATCTTCCAGATCAATATGATC 908
Db 361 GTGATGTAGTGGTTTGGACTCTTCCCAGGAAATTCATCTTCCAGATCAATATGATC 420
OY 909 AAGTACATCAAGACAAATACCCCTAATCTCCAAAGTCATTTGAGGCAATGTGTCACCTCT 968
Db 421 AAGTACATCAAGACAAATACCCCTAATCTCCAAAGTCATTTGAGGCAATGTGTCACCTCT 480
OY 969 GCCCAGGCCAAGAACCTCATTTGATGCAGGTGTGATGCCCTGGGGTGGGCATGGGAAGT 1028
Db 481 GCCCAGGCCAAGAACCTCATTTGATGCAGGTGTGATGCCCTGGGGTGGGCATGGGAAGT 540
OY 1029 GGCTCCATCTGCATTTATCCAGAGAGTGCTGGCCTGTGGCGGCCCAAGCAACAGAGTG 1088
Db 541 GGCTCCATCTGCATTTACGCAGGAAGTGCTGGCCTGTGGCGGCCCAAGCAACAGAGTG 600
OY 1089 TACAAGTGTATGAGTATGCACGGCGCTTTGGTTCGGTCATTTGCTGATGAGAGATC 1148
Db 601 TACAAGTGTATGAGTATGCACGGCGCTTTGGTTCGGTCATTTGCTGATGAGAGATC 660
OY 1149 CAAATGTGGGTATATTCGCAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGC 1208
Db 661 CAAATGTGGGTATATTCGCAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGC 720
OY 1209 TCTCTCTGGCTGCCACCACTGAGGCCCTTGTGAATACTTCTTTCCGATGGATCCGG 1268
Db 721 TCTCTCTGGCTGCCACCACTGAGGCCCTTGTGAATACTTCTTTCCGATGGATCCGG 780
OY 1269 CTAAGAAATATTCGCGGTATGGGTTCTCTCGATGCCATGACAAAGCCTCAGACGCGAG 1328
Db 781 CTAAGAAATATTCGCGGTATGGGTTCTCTCGATGCCATGACAAAGCCTCAGACGCGAG 840
OY 1329 AACAGATATTTCAGTGAAGCTGACAAATCAAAAGTGCCCAAGGAGTGTCTGGTCTGTG 1388
Db 841 AACAGATATTTCAGTGAAGCTGACAAATCAAAAGTGCCCAAGGAGTGTCTGGTCTGTG 900
OY 1389 CAGGACAAAGGTCATCCACAAATTTGTCCCTTACCCTGATTCCTGGCATCCAAACACTCA 1448
Db 901 CAGGACAAAGGTCATCCACAAATTTGTCCCTTACCCTGATTCCTGGCATCCAAACACTCA 960
OY 1449 TGCCAGACATTTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGAG 1508
Db 961 TGCCAGACATTTGGTCCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGAG 1020
OY 1509 CTTAAGTTTGAAGAAGACGTCCTCAGCCCAAGGTGGAAGGTGGCTCCATAGCCTCCAT 1568
Db 1021 CTTAAGTTTGAAGAAGACGTCCTCAGCCCAAGGTGGAAGGTGGCTCCATAGCCTCCAT 1080
OY 1569 TCGTATGAGAAAGCGGCTTTCTGAAAAGGGATCCAGACACACCTCGGTTTCTTTTCA 1628
Db 1081 TCGTATGAGAAAGCGGCTTTCTGAAAAGGGATCCAGACACACCTCGGTTTCTTTTCA 1140
OY 1629 ATAAAAGTTTGAAGAAG 1644
Db 1141 ATAAAAGTTTGAAGAAG 1156
RESULT 9
ABK83782
ID ABK83782 standard; cDNA; 2858 BP.
XX
AC ABK83782;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #353.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;

||||| 1730 TGGCCCTTGAGAGCCTCCACAGTGAATGATGGGCTCCCTGTGCGCCGCCACTACGAGGCC 1789
QY 1237 CTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTC 1296
Db 1790 CTGGCGAGTACTTCTTCTCAGACCGGGGTGCGGCTCAAGAAGTACGGGGCATGGGCTCAC 1849
QY 1297 TCGATGCCATGAGACACACCTCAGACGCCAGAACAGATATTCAGTGAAGCTGACAAAA 1356
Db 1850 TGGATCCCATGAGAGAGAGACAGACAGCCAGAAAGATACTTCAGCGAGGGGATAAAG 1909
QY 1357 TCAAGTGGCCAGGAGGTGTCTGTCTGTCTGTGACGAGACAAGGCTCAATCCACAATTTC 1416
Db 1910 TGAAGATCGACACAGGGTGTCTCGGGCTCCATCCAGGACAAAGATCCATTCAAGAATTGC 1969
QY 1417 TCCCTTACCTGATTTGCTGGCATCCACACTCATGCCAGACATTGTCCTCAAGAGCTTGA 1476
Db 1970 TGCCCTACCTCATATGACAGGCATCCAAACAGGCTGCCAGATATCGGGGCCCGCAGCCTGT 2029
QY 1477 CCCAAGTCCGAGCCATGATGTACTCTGGGAGCTTAAGTTTGAGAAGAGAAGCTCCTCAG 1536
Db 2030 CTGTCTTCGGGTCCATGATGTACTAGAGAGAGCTCAAGTTTGAGAAGCGGACCATGTGCG 2089
QY 1537 CCCAGTGGGAAGGTGGCGTCCATAGCCTCCATTCGTATGAGAAGCGGCTTTTCTGA 1592
Db 2090 CCCAGATTGAGGGTGTGTCCATGGCTGCACCTCTTACGAAAGCGGCTGTACTGA 2145
RESULT 10
ABN95621
ID ABN95621 standard; DNA; 2858 BP.
XX AC ABN95621;
DT 13-AUG-2002 (first entry)
XX De Gene #2119 used to diagnose liver cancer.
XX Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX OS Homo sapiens.
XX PN WO200229103-A2.
XX PD 11-APR-2002.
XX PF 02-OCT-2001; 2001WO-US30589.
XX PR 02-OCT-2000; 2000US-237054P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX DR WPI; 2002-426119/45.
XX PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -
XX PS Claim 1; SEQ ID NO 2119; 298pp; English.
XX CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic

CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX SQ Sequence 2858 BP; 545 A; 923 C; 860 G; 530 T; 0 other;
Query Match 58.1%; Score 960.8; DB 24; Length 2858;
Best Local Similarity 76.1%; Pred. No. 2e-283;
Matches 1184; Conservative 0; Mismatches 372; Indels 0; Gaps 0;
QY 37 CTGTGTTGCCATGGCCGACTACCTGATTAGTGGGGGCACGTCCTACGTGCCAGACGACG 96
Db 590 CAGGGCTAGCCATGGCGGACTACCTGATCAGCGCGGCGACCGGCTACGTCGCCGAGATG 649
QY 97 GACTCAGACACAGCAGCTCTTCAACTGCGGAGACGGCCTCACCTTACATGACTTTCTCA 156
Db 650 GGCTCACCGCGCAGCAGCTCTTCGCCAGCGCCGACGACCTCACCTACAGACTTCTCTGA 709
QY 157 TTCTCCCTGGGTACATCGACTTCACCTGCAGACCAAGGTGACCTGACTTCTGCTCTGACA 216
Db 710 TTCTCCAGGATTCATAGACTTCACTGATGAGGTGACCTGACCTGACCCCTGACCC 769
QY 217 AGAAATCACTCTTAAGACCCCACTGGTTTCTCTCTCCATGACACACAGTCACAGAGCTG 276
Db 770 GGAAGATCACGCTGAAGACGCCACTCATCTCTCCGCCATGACACCTGTGACAGAGGCTG 829
QY 277 GGATGCCATAGCAATGGCGCTTACAGCGCGGTATTTGGCTTCATCCACCACTGTACAC 336
Db 830 ACATGGCCATTGCCATGGCTGTGATGGAGGTATTTGGTTCACTTCAACCAACTGCACCC 889
QY 337 CTGAATTCAGGCCCAATGAAGTTGCGAAATGAAGAAATATGAACAGGATTCATCACAG 396
Db 890 CAGAGTTCAGGCCCAATGAAGTACGCAAGGTCAAGAACCTTGAACAGGGCTTCATCACGG 949
QY 397 ACCCTGTGCTCTCAGCCCCCAAGGATCGCGTGGGATGTTTTTGAAGCCCAAGCGCCGGC 456
Db 950 ACCCTGTGCTCTGAGCCCCCTCGCACACTGTGGCGATGTGCTGGAAGGCCAAGATGGCGC 1009
QY 457 ATGTTTCTCGGGTATCCCAATCACACACACAGCGCCGATGGGAGCCGCTTGTGTGGCA 516
Db 1010 ATGCTTCTCTGGCATCCCATCTACTGAGACGGGACCATGGGCAAGCTGTGTGGCA 1069
QY 517 TCATCTCTCCAGGGACATGATTCTTCAAGAGAGGAAGACATGACTGTTCTTTGGAAG 576
Db 1070 TCGTCACTCCGAGACATGACTTCTTCTGTGAGAAGGACCAACCACTCTCTCAGTG 1129
QY 577 AGATAATGACAAAGAGGGAAGACTGTGTAGCCCCCGCAGCATCACACTGAAGAGG 636
Db 1130 AGGTGATGACGCCAAGGATGAAGTGTGTGCTCCAGCAGCTGTGACGTTGAAGAGG 1189
QY 637 CAAATGAATTTCTGCAGCGCAGCAAGAGGAAGTTGCCAATTGTAATGAAGATGATG 696
Db 1190 CAAATGAGATCTCGACGCTAGCAGAAAGGAAGCTGCCATCTCATGATTTGCGATG 1249
QY 697 AGCTTGTGGCCATCATTTGCCCGGACAGACCTGAAGAAGATCGGACTACCCACTAGCCT 756
Db 1250 AGCTGTGGCCATCATTCGCCCCGACCGACCTGAAGAAGATCGAGACTAACCTCTGGCCT 1309
QY 757 CCAAGATGCCAAGAAACAGCTGTGTGTGGGGCAGCCATTGGCACTCATGAGATGACA 816
Db 1310 CCAAGATTCGCCAAGACAGCTGTCTGTGGGGCAGCTGTGGCACCCTGAGATGACA 1369
QY 817 AGTATAGCTGGAATTTGCTCGCCACGCTGTGTGATGTAGTGGTTTGGACTCTTCCC 876
Db 1370 AATACCGTGTGAACCTGCTGACCCAGCGGGGCTGACGTCACTAGTCTTCCACTGTCCC 1429
QY 877 AGGGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAGACAATACCTAATC 936
Db 1430 AAGGAATTGGGTGTATCAGATCGCCATGTGTGATTTACATCAACAGAAAGTACCCCAAC 1489

QY 937 TCCAGTCATTGGAGCAATGTGCTCAGTCTGCCCCAGGCCAAGAACCTCATTTGATGACAG 996
1111 11 11111 11 11 11111 11 11 111111111111 11 1111111 1
Db 1490 TCCAGGTGATTGGGGGAACGTGGTGACAGACAGCCAGGCCAAGAACCTGATTGATGCTG 1549
QY 997 GTGTGATGCCCTGCGGGTGGCATGGGAAGTGGCTCCATCTGCATTAATCCAGGAAGTGC 1056
111111 1 1111 1111111111 1 1111111111 1 1111111111
Db 1550 GTGTGACGGGCTGCGGTGGGCATGGGCTGCGGCTCCATCTGCATCAATCCAGGAAGTGA 1609
QY 1057 TGGCTGTGGGGCGGCCCAAGCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCGCT 1116
111111111 1111111 1 11 11 111111111 111111 111111 111111
Db 1610 TGGCTGTGTGCGGCCCAAGGCACTGTGTGTACAAAGTGGCTGAGTATGCCCGCGCT 1669
QY 1117 TTGGTGTCCGGTCAATGTGATGAGGAATCCAAATGTGGGTCAATATTCGGAAGCCT 1176
111111 11 1111 11 1111 11 1111 1 1111 1 11 11 11
Db 1670 TTGGTGTCCCATCATAGCCGATGCGGCATCCAGACCCTGGGACACCTGGTCAAGGCC 1729
QY 1177 TGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCGGCTGCCAATCACTGAGGCC 1236
111111111 11111111 11111111 11 1111 1111 11 111111
Db 1730 TGGCCCTTGGAGCCTCCACAGTGAATGATGGCTCCCTGTGGCGCCCACTACGAGGCC 1789
QY 1237 CTGGTGAATACCTTCTTTCCGATGGATCCGGCTAAAGAAATATCGCGTATGGGTTCTC 1296
1111 11 111111 11 11 1111 1 1111 1111 11 11 1111 11 1
Db 1790 CTGGGAGTACTTCTTCTCAGCGGCTGCGGCTCAAGAAATACCGGTCATGGGCTCAC 1849
QY 1297 TCGATGCCATGGACAAGCACCTCAGCAGCCAGAACAGATATTTCAAGTGAACAA 1356
1 111 111111 111 1 111111111 111 1111 1 11 11
Db 1850 TGGATGCCATGGAGAAGAGAGAGCAGCAGCCAGAAACGATACTCAGCGTAGGGGATAAG 1909
QY 1357 TCAAGTGGCCAGGAGTGTGCTGTGTGACAGACAAGGCTCAATCCACAATTTG 1416
1 11 11 11111 11 11 11 11111111 11 11 11 11 11 11 1
Db 1910 TGAAGATCGACAGGTTGTCTGCGGCTCCATCCAGGACAAGGATCCAATCAGAAGTTGC 1969
QY 1417 TCCCTTACCTGATTTGCTGGCATCCAACACTCATGCGAGACATTTGTCACAGAGCTTGA 1476
1 11 11111 11 11 111111111 111111 11 11 11 11 11 11
Db 1970 TGCCCTAACCTCATAGCAGGCATCCAAACAGCGCTGCCAGATATCGGGTCCCGACCTGT 2029
QY 1477 CCCAAGTCCGAGCCATGATGTACTCTGGGGAGCTTAAGTTTGAGAGAGAATACCTCCTCAG 1536
1 1 11 1111111111 11 1111 111111111 11 11 11
Db 2030 CTGTCTTCGGTCCATGATGTACTCAGAGAGCTCAAGTTTGAGAGAAGGACCATGTGCG 2089
QY 1537 CCCAGGTGAAGGTGGCGTCCATAGCCCTCCATTCGTATGAGAACCGGCTTTTCTGA 1592
11111 11 11111 11111 1111 11 11 11 111111 1 1111
Db 2090 CCCAGATTGAGGTTGTGTCCATGGCCCTGCACCTCTTACGAATAAGCGGGCTACTGA 2145

RESULT 11
AAS86456
ID AAS86456 standard; cDNA; 3387 BP.
XX AAS86456;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX DNA encoding novel human diagnostic protein #22260.
DE
XX
KW Human; chromosome mapping; gene mapping; gene therapy forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001: 2001WO-US08631.
XX
PR 31-MAR-2000: 2000US-0540217.
PR 23-AUG-2000: 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;

XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG22269.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 22260; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations in
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3387 BP; 677 A; 1065 C; 988 G; 653 T; 0 other;

Query Match 52.3%; Score 865.6; DB 23; Length 3387;
Best Local Similarity 74.6%; Pred. No. 3.5e-254;
Matches 1167; Conservative 0; Mismatches 389; Indels 8; Gaps 6;

QY 37 CTGTGTTGGCCATGGCGCACTACCTGATTAAGTGGGGACACGTCCTAGTGCCAGACGACG 96
1 1 1 1111111 111111111 11 11 1111 1111111 11 11 1
Db 1077 CAGGGCTAGCCATGGCGGCACTACCTGATCAAGCGGGCACCGGCTACGTGCCGAGCATG 1136
QY 97 GACTCAGACACAGCAGCTCTTCAACTGCGGAGACGGGCTCACTACAATGACTTTCTCA 156
1 1111 11 111111111 1 111 111 111111111 1111 11 1
Db 1137 GGCTCACCGCGCAGCAGCTCTTCCGACGCGCCGAGACCTCACTACAACGACTTCTGA 1196
QY 157 TTCTCCCTGGGTACATGCACTTCACTGCAGACCAAGGTGACCTGACTTCTGTGACCA 216
111111 11 111 111111 11 11 111111111 11 11 11111
Db 1197 TTCTCCAGGATTCAATAGACTTCAAGCTGATGAGGTGACCTGACCTCAGCCCTGACCC 1256
QY 217 AGAAATCACTCTTAAGACCCCACTGTTCTCTCCATGAGACAGATCAGAGAGGCTG 276
111 1111 11 11111 1111 1 1111 111111111 11 11111111
Db 1257 GGAAGATCACGCTGAAGACGCGCACTCATCTCCCCCATGAGACATGTGACAGAGGCTG 1316
QY 277 GGATGGCCATAGCAATGCGGCTTACAGGCGGTATTGGCTTCATCCACCACAACCTGTACAC 336
111111 11 1111 11 11 111111 1111 11111111 11 11
Db 1317 ACATGGCCATTGCAATGAGTGGATGGAGGTATTGGGTTCATTACCAACAACCTGACCC 1376
QY 337 CTGAATTCAGGCAATGAAGTTCGGAAGTGAAGAAATATGAACAGGATTCATCAGAG 396
1 11 111111111 11111 11 11 1111 1 111111 1111111 1
Db 1377 CAGAGTTCCAGGCCAATGAAGTACGCAAGGTCAAGAACTTTGAACAGGCTTCATCAGCG 1436
QY 397 ACCCTGTGCTCTCAGCCCAAGGATCGGTGCGG-GATGTTTTTGAGGCCAAAGCCCGG 455
111111111 111111 1 111 11 1111 1 1111 1111 111
Db 1437 ACCCTGTGCTGTGAGCCCTCGCACACTGTGGGCGGATGCTGAGGGCAAGATCGCG 1496
QY 456 CATGCTTCT-GCGGTATCCCAATCACAGACACAGGCGGATGGGAGCGCTGTGCGG 514
1111 1111 11 1111 1111 11 11 111 1111 111 111111
Db 1497 CATGCTTCTGTGGCATCCCATCATCTGAGACCGGACCATGGCAGCAAGCTGTGCGG 1556
QY 515 CATCATCTCTCCAGGAGACATGATTTTCTCAAGAGAGGAACATGACTGTTCTTGA 574
1111 11 1111 1 1111 11 1111 111 1111 11 11 1

Db	1557	CATCGTCACCTCCCGAGACATCGACTTCTTGGTGAGAGGACCACACCCTCTCAG	1616
OY	575	AGAGATAATGACAAAGAGGAGACTTGGTGGTAGCCCCCGCAGCATCACACTGAAGGA	634
Db	1617	TGAGGTGATGACGCCAAGGATGAACGTGGTGGTCCAGCAGGTGTGACGTTGAAGA	1676
OY	635	GGCAAAATGAAATTTCTGCAGCGCGCAAGGAGGAAAGTTGCCATTGTAAATGAAGATGA	694
Db	1677	GGCAAAATGAGATCTCTGCAGCGTAGCAAGAAAGGAAGCTGCTTATCGTCAATGATTGCGA	1736
OY	695	TGAGCTTGTGGCCATCATTTGCCGGACAGACCTGAAGAAGAAATCGGACTACCCACTAGC	754
Db	1737	TGAGCTGGTGGCCATCATCGCCCGCACCGACCTGAAGAAGCCGAGACTACCTCTGGC	1796
OY	755	CTCCAAGATGCCAAGAACAGCTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGA	814
Db	1797	CTCCAAGGATTTCCAGCCGAGCTCTCTGTGGGGCAGCTGTGACACACCCGTGAGGAGA	1856
OY	815	CAAGTATAGGCTGGACTTGCCTCGCCCAAGGCTGGTGTGATGTAGTGGTTTGGACTCTTC	874
Db	1857	CAAAATACCGTCTGGACCTGCTACCCAGCGGGCGGTGACGTCATAGTCTTGGACTCGTC	1916
OY	875	CCAGGGAATTTCCATCTTCCAG-ATCAATATGATCAAGTACATCAAGACAATACCCTA	933
Db	1917	CCAAGGGAATTCGGTGTATCAGTACCGCCAGGGTGTCTTACTTCAAAACAGAAGTACCCCC	1976
OY	934	ATCTCCAAGT-CATTGAGGCAATGTGTCACTGCTGCCCGCCCAAGACCTCATTTGAT	992
Db	1977	ACCTCCAGGTGTATGGGGGAACTGGTGACAGCAGCCAGCCCAAGAACCTGATTTGAT	2036
OY	993	GCAGTGTGGATGCCCTGCGGGTGGGCATGGGAAGTGGCTCCATCTGCATTATCCA-GGA	1051
Db	2037	GCTGGTGGACGGGCTGCCGCTGGGCATGGGCTGCCGCTCCATCTGCATCACCCAGGGA	2096
OY	1052	AGTGTGGCTGTGGGGGGCCCCCAACAAC--AGCAGTGTACAAGGTGTATGAGTATGC	1108
Db	2097	AGTATGGCCTGTGGTGGCCCCCAGGGCAGCTTGTGTATTCAAGGTAGGCTGAGTATGC	2156
OY	1109	ACGGCGCTTTGGTGTCCGGTCAATTGCTGATGGAGGAATCCAAATGTGGGTCAATATGC	1168
Db	2157	CCGGCGCTTTGGTGTGCCCATCATAGCCGATGGCGGCATCCAGACCGTGGACACGTGCT	2216
OY	1169	GAAAGCCTTGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCTGGCTGCCACAC	1228
Db	2217	CAAGCCCTGGCCCTTGAGCCCTCACAGTATGATGGGCTCCTCTGTGGCCGCACTTAC	2276
OY	1229	TGAGCCCCCTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATATCGCGGTAT	1288
Db	2277	GGAGCCCCCTGGCGAGTACTTCTTCTCAGACGGGGTGGGCTCAAGAAGTACCGGGCAT	2336
OY	1289	GGTTCCTCTCGATGCCATGGACAAGCAGCTCAGCAGCCAGAACAGATATTTAGTGAAGC	1348
Db	2337	GGGCTACTGGATGCCATGGAGAAGCAGCAGCAGCAGAAACGATACTTCAGCGAGGG	2396
OY	1349	TGACAAAATCAAAAGTGGCCAGGGAGTGTCTGTGCTGTGCAGAGCAAAAGGTCATCCA	1408
Db	2397	GGATAAGTGAAGATCGCGCAGGGTGTCTCGGGCTCCATCCAGGACAAAGATTCATTCA	2456
OY	1409	CAAAATTTGCTCCCTTACCTGATTGCTGGCATCCAAACACTCATGCCAGACATTTGGTCCAA	1468
Db	2457	GAAGTTCGTGCCCTTACCTCATAGCAGGCATCCAACACGGCTGCCAGGATATCGGGCCCG	2516
OY	1469	GAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGGAGCTTAAGTTGAGAAGAGAAC	1528
Db	2517	CAGCTGTCTGTCTTCCTTCGATCATGATGTACTCAGGAGAGCTCAAGTTTGAGAAGCGAC	2576
OY	1529	GTCCTCAGCCAGGTGGAAGGTGGCTCCATAGCCTCCATTCGTATGAGAAGCGGCTTTT	1588
Db	2577	CATGTGCGCCCAGATTTGAGGGTGGTGTCCATGGCCTGCACCTTTACGAAAAAGCGGCTGA	2636
OY	1589	CTGA 1592	
Db	2637	CTGA 2640	

RESULT 12	
AAD28929	
ID	AAD28929 standard; DNA; 1158 BP.
XX	
AC	AAD28929;
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	Human type II IMPDH-SPTQ variant DNA.
XX	
KW	Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery;
KW	proliferative-type disease; cancer; imaging methodology; cytostatic;
KW	therapy; enzyme; variant; ds.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200185952-A2.
XX	
PD	15-NOV-2001.
XX	
XX	10-MAY-2001; 2001WO-US15457.
PF	
XX	
PR	10-MAY-2000; 2000US-203448P.
XX	
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Krystek SR, Sheriff S, Wilmer MR, Hollenbaugh DL, Yan N;
PI	Mouravieff JE, Einspahr HM, Kish K;
XX	
DR	WPI; 2002-164105/21.
XX	
PT	New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT	having an oligo-peptide domain substituted for a subdomain of a
PT	wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT	antibodies -
XX	
PS	Claim 54; Fig 12; 161pp; English.
XX	
CC	The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC	(IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC	substituted for a subdomain of a wild-type IMPDH polypeptide. The
CC	modified IMPDH polypeptides are useful for drug discovery, for
CC	therapeutic, diagnostic and prognostic procedures for detecting or
CC	quantifying modified IMPDH polypeptides and their corresponding nucleic
CC	acids. IMPDH polypeptides are also useful for generating antibodies, as
CC	diagnostic and prognostic markers of diseases, as targets for various
CC	therapeutic modalities, and to identify and isolate ligands and other
CC	agents that bind to modified IMPDH. These antibodies may be used in the
CC	diagnostic assays, imaging methodologies, therapeutic methods in the
CC	management of cancer or other proliferative-type diseases, and in
CC	purifying modified IMPDH polypeptides and for isolating related
CC	molecules such as wild type and mutant IMPDH polypeptides. The present
CC	sequence is human type II IMPDH-SPTQ variant DNA.
XX	
SQ	Sequence 1158 BP; 279 A; 301 C; 310 G; 268 T; 0 other;
Query Match	49.4%; Score 816.4; DB 24; Length 1158;
Best Local Similarity	98.7%; Pred. No. 2.2e-239;
Matches 823; Conservative	0; Mismatches 11; Indels 0; Gaps 0;
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Db	325 AAATATTTCTCCGACTCAGCTGCTGTGGGGCAGCCATTTGGCACTCATGAGATGACAAG 384
OY	819 TATAGGCTGGAAGCTTCTGCTGCGCCAGGCTGGTGTGATGTAGTGGTTTGGACTCTTCCAG 878
Db	385 TATAGGCTGGAAGCTTCTGCTGCGCCAGGCTGGTGTGATGTAGTGGTTTGGACTCTTCCAG 444
OY	879 GGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAGACAATACCTTAATCTC 938

Db 445 GGAATTCCATCTTCCAGATCAATATGATCAAGTACATCAAGACAAATACCCCTAATCTC 504
QY 939 CAAGTCATTTGGAGGCAATGTGTCACCTGCTGCCAGGCCAAGACCTGATTGATGCAGGT 998
Db 505 CAAGTCATTTGGAGGCAATGTGTCACCTGCTGCCAGGCCAAGACCTGATTGATGCAGGT 564
QY 999 GTGGATGCCCTGGGGTGGGATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGC 1058
Db 565 GTGGATGCCCTGGGGTGGGATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGC 624
QY 1059 GCCCTGGGGCGGGCCCCCAAGCAACAGCAGTGTACAAGGTGTATGAGTATCCACGGGCTTT 1118
Db 625 GCCCTGGGGCGGGCCCCCAAGCAACAGCAGTGTACAAGGTGTACAGAGTATCCACGGGCTTT 684
QY 1119 GGTGTTCCGGTCATTTGCTGATGGAGAAATCCAAATGTGGGTCAATATCCGAAAGCCTTG 1178
Db 685 GGTGTTCCGGTCATTTGCTGATGGAGAAATCCAAATGTGGGTCAATATATCCGAAAGCCTTG 744
QY 1179 GCCCTGGGGCGCTCCACAGTCATGATGGGCTCTCTCCTGGCTGCCACCACTGAGGCCCT 1238
Db 745 GCCCTGGGGCGCTCCACAGTCATGATGGGCTCTCTCCTGGCTGCCACCACTGAGGCCCT 804
QY 1239 GGTGATACTTCTTTTCCGATGGATCCGGCTAAAGAAATATCCGGGTATGGGTCTCTC 1298
Db 805 GGTGAATACTTCTTTTCCGATGGATCCGGCTAAAGAAATATCCGGGTATGGGTCTCTC 864
QY 1299 GATGCCATGGACAAGCACCCTCAGCAGCCAGAACAGATATTTACGTGAATCTGACAAATC 1358
Db 865 GATGCCATGGACAAGCACCCTCAGCAGCCAGAACAGATATTTACGTGAATCTGACAAATC 924
QY 1359 AAAGTGGCCCCAGGAGTGTCTGTGCTGTGTCAGAGACAAAGGTCATCCACAAATTTGTC 1418
Db 925 AAAGTGGCCCCAGGAGTGTCTGTGCTGTGTCAGAGACAAAGGTCATCCACAAATTTGTC 984
QY 1419 CCTTACCTGATTGCTGGCATCCAACTCATGCCCAGAGACATTTGGTCCCAAGAGCTTGACC 1478
Db 985 CCTTACCTGATTGCTGGCATCCAACTCATGCCCAGAGACATTTGGTCCCAAGAGCTTGACC 1044
QY 1479 CAAGTCGAGCCATGATGTACTCTGGGGAGCCTTAAGTTTGAGAGAGAGACGTCCCTCAGCC 1538
Db 1045 CAAGTCGAGCCATGATGTACTCTGGGGAGCCTTAAGTTTGAGAGAGAGACGTCCCTCAGCC 1104
QY 1539 CAGGTGGAAGGTGGCGTCCATAGCCTCCATTGCTATGAGAAAGCGCTTTTCTGA 1592
Db 1105 CAGGTGGAAGGTGGCGTCCATAGCCTCCATTGCTATGAGAAAGCGCGCTTTTCTGA 1158

RESULT 13
AAD28927
ID AAD28927 standard; cdna; 1158 BP.
XX
AC AAD28927:
XX
DT 07-MAY-2002 (first entry)
XX
DE Human type II IMPDH-AGRP variant cDNA.
XX
KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH; drug discovery; proliferative-type disease; cancer; imaging methodology; cytostatic; therapy; enzyme; variant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT CDS 1..1158 location/Qualifiers
FT /*tag= a
FT /product= "Human type II IMPDH-AGRP variant"
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PN WO200185952-A2.
XX
PD 15-NOV-2001.

PF 10-MAY-2001: 2001WO-US15457.
XX
PR 10-MAY-2000; 2000US-203448P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Krystek SR, Sheriff S, Wilmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;
XX
DR WPI: 2002-164105/21.
DR P-PSDB: AAEL18181.
XX
PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide having an oligo-peptide domain substituted for a subdomain of a wild-type IMPDH polypeptide, useful in drug discovery or for generating antibodies
XX
PS Claim 54; Fig 14; 161pp; English.
XX
CC The invention relates to modified inosine 5'-monophosphate dehydrogenase (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain substituted for a subdomain of a wild-type IMPDH polypeptide. The modified IMPDH polypeptides are useful for drug discovery, for therapeutic, diagnostic and prognostic procedures for detecting or quantifying modified IMPDH polypeptides and their corresponding nucleic acids. IMPDH polypeptides are also useful for generating antibodies, as diagnostic and prognostic markers of diseases, as targets for various therapeutic modalities, and to identify and isolate ligands and other agents that bind to modified IMPDH. These antibodies may be used in diagnostic assays, imaging methodologies, therapeutic methods in the management of cancer or other proliferative-type diseases, and in purifying modified IMPDH polypeptides and for isolating related molecules such as wild type and mutant IMPDH polypeptides. The present sequence is human type II IMPDH-AGRP variant cDNA.
SQ Sequence 1158 BP; 277 A; 300 C; 313 G; 268 T; 0 other;

Query Match 49.2%; Score 813.2; DB 24; Length 1158;
Best Local Similarity 98.4%; Pred. No. 2.1e-238;
Matches 821; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 759 AAAGATGCCAAGAAGACAGCTGCTGTGTGGGGCAGCCATTGGCAGCTCATGAGGATGACAAG 818
Db 325 AAATATGCTGTGTCGTCGCTGTGTGGGGCAGCCATTGGCAGCTCATGAGGATGACAAG 384
QY 819 TATAGGCTGGACTTGTCTGGCCAGCGCTGGTGTGATGTAGTGTGTTGGACTCTTCCAG 878
Db 385 TATAGGCTGGACTTGTCTGGCCAGCGCTGGTGTGATGTAGTGTGTTGGACTCTTCCAG 444
QY 879 GGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAGACAATACCCTAATCTC 938
Db 445 GGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAGACAATACCCTAATCTC 504
QY 939 CAAGTCATTGGAGGCAATGTGTGCTGCTGCCAGGCCAAGACCTCATTTGATGCAGGT 998
Db 505 CAAGTCATTGGAGGCAATGTGTGCTGCTGCCAGGCCAAGACCTCATTTGATGCAGGT 564
QY 999 GTGGATGCCCTGGGGTGGGATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGC 1058
Db 565 GTGGATGCCCTGGGGTGGGATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGC 624
QY 1059 GCCCTGGGGCGGGCCCCAAGCAACAGCAGTGTACAAGGTGTATGAGTATCCACGGGCTTT 1118
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QY 1119 GGTGTTCCGGTCATTTGCTGATGGAGAAATCCAAATGTGGGTCAATATCCGAAAGCCTTG 1178
Db 685 GGTGTTCCGGTCATTTGCTGATGGAGAAATCCAAATGTGGGTCAATATCCGAAAGCCTTG 744
QY 1179 GCCCTGGGGCGCTCCACAGTCATGATGGGCTCTCTCCTGGCTGCCACCACTGAGGCCCT 1238
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QY	1239	GGTGAATACTTCTTTTCCGATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTC	1298
Db	805	GGTGAATACTTCTTTTCCGATGGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCTC	864
QY	1299	GATGCCATGACAAACACCTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATC	1358
Db	865	GATGCCATGACAAACACCTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAATC	924
QY	1359	AAAGTGGCCACAGGAGTGTCTGTGCTGTGCAGGACAAAGGGTCAATCCACAAATTTGTC	1418
Db	925	AAAGTGGCCACAGGAGTGTCTGTGCTGTGCAGGACAAAGGGTCAATCCACAAATTTGTC	984
QY	1419	CCTTACCTGATTTGCTGGCATCCAAACACTCATGCCAGACATTTGGTGCCAAAGACTTGACC	1478
Db	985	CCTTACCTGATTTGCTGGCATCCAAACACTCATGCCAGACATTTGGTGCCAAAGACTTGACC	1044
QY	1479	CAAGTCCGAGCCATGATGTACTCTGGGGAGCTTAAGTTTGAGAAGAGAAGACGTCCTCAGCC	1538
Db	1045	CAAGTCCGAGCCATGATGTACTCTGGGGAGCTTAAGTTTGAGAAGAGAAGACGTCCTCAGCC	1104
QY	1539	CAGGTGAAGGTGGGGTCCATAGCCTCCATTGCTATGAGAAGCGGCTTTTCTGA	1592
Db	1105	CAGGTGAAGGTGGGGTCCATAGCCTCCATTGCTATGAGAAGCGGCTTTTCTGA	1158

RESULT 14
AAD28928

AC AAD28928;

DT 07-MAY-2002 (first entry)

DE Human type II IMPDH-NSPL variant cDNA.

KW Human; inosine 5'-monophosphate dehydrogenase; IMPDH, drug discovery;
KW proliferative-type disease; cancer; imaging methodology; cytostatic;
KW therapy; enzyme; variant; ss.

OS	Homo sapiens.
OS	Synthetic.

Key	Location/Qualifiers
FH	1..1158
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FT	/tag= a
FT	/product= "Human type II IMPDH-NSPL variant"

PN WO200185952-A2

PD 15-NOV-2001

PF 10-MAY-2001; 2001WO-US15457.

PR 10-MAY-2000; 2000US-203448P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Krystek SR, Sheriff S, Witmer MR, Hollenbaugh DL, Yan N;
PI Mouravieff JE, Einspahr HM, Kish K;

DR WPI; 2002-164105/21.
DR P-PSDB; AAE18183.

PT New modified inosine 5'-monophosphate dehydrogenase (IMPDH) polypeptide
PT having an oligo-peptide domain substituted for a subdomain of a
PT wild-type IMPDH polypeptide, useful in drug discovery or for generating
PT antibodies -

PS Claim 54; Fig 16; 161pp; English.

CC The invention relates to modified inosine 5'-monophosphate dehydrogenase
CC (IMPDH; EC 1.1.1.205) polypeptide, comprising an oligo-peptide domain
CC substituted for a subdomain of a wild-type IMPDH polypeptide. The

modified IMPDH polypeptides are useful for drug discovery, for therapeutic, diagnostic and prognostic procedures for detecting or quantifying modified IMPDH polypeptides and their corresponding nucleic acids. IMPDH polypeptides are also useful for generating antibodies, as diagnostic and prognostic markers of diseases, as targets for various therapeutic modalities, and to identify and isolate ligands and other agents that bind to modified IMPDH. These antibodies may be used in diagnostic assays, imaging methodologies, therapeutic methods in the management of cancer or other proliferative-type diseases, and in purifying modified IMPDH polypeptides and for isolating related molecules such as wild type and mutant IMPDH polypeptides. The present sequence is human type II IMPDH-NSPL variant cDNA.

Sequence 1158 BP; 279 A; 301 C; 309 G; 269 T; 0 other;

Query match	49.08;	Score 810;	DB 24;	Length 1158;
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Matches	819;	Conservative	0;	Mismatches	15;	Indels	0;	Gaps	0;
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Dd	325	AAATATAACTCTCCGCTTCTGCTGTGTGGGCAGCCATTGGCACTCATGAGGATGACAAG	384
QY	819	TATAGGCTGGACTTGCTCGCCCCAGCGCTGGTGTGGATGTACTGGTTTGGACTCTTCCAG	878
Dd	385	TATAGGCTGGACTTGCTCGCCCCAGCGCTGGTGTGGATGTACTGGTTTGGACTCTTCCAG	444

QY 879 GGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAAGACAATAATACCCTAATCTC 938
+ + + + +
Db 445 GGAATTCATCTTCCAGATCAATATGATCAAGTACATCAAAGACAATAATACCCTAATCTC 504

Qy 939 CAAGTCATTGGAGGCCAATGTGGTACTGCTGCCAGGCCAAGAACCCTCATTTGATGCAGGT 998
|||||
Db 505 CAAGTCATTGGAGGCCAATGTGGTACTGCTGCCAGGCCAAGAACCCTCATTTGATGCAGGT 564
|||||

```
Qy    999 GTGATGCCCTGC CGGTGGCCATGGGAAGTGGCTTCATCTGCATTATCCAGGAAGTGCTG 1058
      |||||
Db    565 GTGGATGCCCTGC CGGTGGCCATGGGAAGTGGCTTCATCTGCATTATCCAGGAAGTGCTG 624
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[illegible]

QY	1119	GGGTGTCGGGTCAATGCTGATGGAGGAATCCAAAATGTGGGTCAATATTGGCAAGCCTTG	1178
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QY	1179	GCCCTTGGGCGCTCCACAGTCATGATGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCT	1238
Db	745	GCCCTTGGGCGCTCCACAGTCATGATGGCTCTCTCCCTGGCTGCCACCACCTGAGGCCCT	804

QY 1239 GGTGATACCTCTTTTCCGATGGGATCCGCTAAAGAAATATCGCGGTATGGCTTCTCTC 1298
 |||||
 Db 805 GGTGATACCTCTTTTCCGATGGGATCCGCTAAAGAAATATCGCGGTATGGCTTCTCTC 864

	QY	1299	GATGCCATGACAACCACTCAGCAGCCAGAACACATAATTTCAGTGAAGCTGACAAATC	1358
Dh		865	GATGCATGACAACCACTTAGCAGCCAGAACACACTTTTTCAGTGAAGCTGACAAAATC	924

QY	1359	AAAGTGGCCAGGAGTGTCTGGTCTGTGCAGAGACAAGGGTCAATCCACAATTTGTC	1418
Dh	925	AAAGTGGCCAGGAGTGTCTGGTCTGTGCAGAGACAAGGGTCAATCCACAATTTGTC	984

QY 1419 CCTACCTGATTGCTGGCATCCAACACTCATGCGCAGACATTGGTGCCAGAGCTTGACC 1478

pb 985 CCTTACCTGATTGCTGGCATCCAACACTCATGCGCAGACATTGGTGCCAGAGCTTGACC 1044

[illegible]

QY 1539 CAGGTGGAAGGTGGCGTCCATAGCCTCCATTGCTATGAGAAGCGGCTTTTCTGA 1592
|||||

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GenCore version 5.1.3
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SUMMARIES

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2	1141.6	69.0	1157	10	US-09-822-849A-48 Sequence 48, Appl
3	960.8	58.1	2858	10	US-09-880-107-2119 Sequence 2119, Ap
4	816.4	49.4	1158	10	US-09-853-918-45 Sequence 45, Appl
5	813.2	49.2	1158	10	US-09-853-918-46 Sequence 46, Appl
6	810	49.0	1158	10	US-09-853-918-47 Sequence 47, Appl
7	809.6	48.9	1155	10	US-09-853-918-40 Sequence 40, Appl
8	809.6	48.9	1155	10	US-09-853-918-41 Sequence 41, Appl
9	809.6	48.9	1155	10	US-09-853-918-42 Sequence 42, Appl
10	809.6	48.9	1155	10	US-09-853-918-43 Sequence 43, Appl
11	655.4	39.6	1851	12	US-10-044-090-65 Sequence 65, Appl
12	545.6	33.0	674	10	US-09-925-302-386 Sequence 386, App
13	513.6	31.1	1155	10	US-09-853-918-44 Sequence 44, Appl
14	420.6	25.4	675	10	US-09-879-536-844 Sequence 844, App
15	410.2	24.8	3616	9	US-10-076-157-7 Sequence 7, Appl1
16	396	23.9	396	9	US-09-970-966-164 Sequence 164, App
17	396	23.9	396	10	US-09-825-294-164 Sequence 164, App
18	328.8	19.9	6193	10	US-09-880-107-2197 Sequence 2197, Ap
19	303	18.3	1512	9	US-09-938-842A-801 Sequence 801, App

20	295.6	17.9	1509	9	US-09-938-842A-800	Sequence 800, App
21	255.6	15.5	1470	10	US-09-815-242-7855	Sequence 7855, Ap
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23	238.2	14.4	435	10	US-09-864-761-4004	Sequence 4004, Ap
24	235.2	14.2	1518	9	US-09-738-626-672	Sequence 672, App
25	222.4	13.4	12022	10	US-09-070-927A-117	Sequence 117, App
26	201.8	12.2	533	10	US-09-864-761-15808	Sequence 15808, A
27	195	11.8	366	10	US-09-864-761-19319	Sequence 19319, A
28	190.4	11.5	294	10	US-09-833-381-765	Sequence 765, App
29	182.6	11.0	1467	10	US-09-815-242-6889	Sequence 6889, Ap
30	180.4	10.9	366	10	US-09-864-761-20764	Sequence 20764, A
31	150	9.1	470	10	US-09-734-017A-75	Sequence 75, Appl
32	132.4	8.0	271	10	US-09-864-761-32316	Sequence 32316, A
33	132	8.0	993	10	US-09-833-381-992	Sequence 992, App
34	115.8	7.0	1062	10	US-09-974-300-577	Sequence 577, App
35	97.2	5.9	1431	9	US-09-738-626-2945	Sequence 2945, Ap
36	83.8	5.1	435	10	US-09-974-300-616	Sequence 616, App
37	83.2	5.0	1483	9	US-10-098-841-20	Sequence 20, Appl
38	83.2	5.0	1525	9	US-10-098-841-21	Sequence 21, Appl
39	81.8	4.9	627	9	US-09-738-626-673	Sequence 673, App
40	75.8	4.6	987	10	US-09-815-242-9163	Sequence 9163, Ap
41	71.2	4.3	1901	10	US-09-925-300-632	Sequence 632, App
42	70	4.2	353	10	US-09-878-574-3520	Sequence 3520, Ap
43	69.4	4.2	617	10	US-09-974-300-6579	Sequence 6579, Ap
44	64	3.9	1044	10	US-09-815-242-9816	Sequence 9816, Ap
45	60	3.6	1044	10	US-09-815-242-5938	Sequence 5938, Ap

ALIGNMENTS

RESULT 1
US-10-044-090-156
: Sequence 156, Application US/10044090
: Patent No. US20020137081A1
: GENERAL INFORMATION:
: APPLICANT: Olga Bandman
: TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
: FILE REFERENCE: PA-0028 US
: CURRENT APPLICATION NUMBER: US/10/044,090
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: PERL Program
: SEQ ID NO 156
: LENGTH: 1633
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No. US20020137081A1 1265962CB1
US-10-044-090-156

Query Match	97.4%	Score 1611;	DB 12;	Length 1633;
Best Local Similarity	99.4%	Pred No. 0;		
Matches 1617;	Conservative	0;	Mismatches 10;	Indels 0;
			Gaps	0;
QY	19	GAGACACGGCGGGTGTCTCTGTGTTGCCATGCGGCGACTGATGATTAGTGGGGCAGCT	78	
Db	1	GAGACACGGCGGGTGTCTCTGTGTTGCCATGCGGCGACTGATGATTAGTGGGGCAGCT	60	
QY	79	CCTACGTGCGAGACGACGAGCTCACAGCAGCAGCTCTTCACTGCGGAGACGGCCTCA	138	
Db	61	CCTACGTGCGAGACGACGAGCTCACAGCAGCAGCTCTTCACTGCGGAGACGGCCTCA	120	
QY	139	CCTACATGACTTTCATTCCTCCCTGGGTACATCGACTTCACCTGCAGACAGGTGACC	198	
Db	121	CCTACATGACTTTCATTCCTCCCTGGGTACATCGACTTCACCTGCAGACAGGTGACC	180	
QY	199	TGACTTCTGCTCTGACCAAGAAATCACTTTAAGACCCCACTGGTTTCTCTCCATGG	258	
Db	181	TGACTTCTGCTCTGACCAAGAAATCACTTTAAGACCCCACTGGTTTCTCTCCATGG	240	
QY	259	ACACAGTCACAGAGGCTGGATGGCCATAGCAATGGCGCTTACAGCGGTTATTGGCTTCA	318	

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Db 241 ACACAGTCACAGAGCGTGGGATGGCCATAGCAATGGCGCTTACAGAGCGGTATTTGGCCCTCA 300
QY 319 TCCACACACTGTACACCTGAATTCACAGGCCAATGAAGTTCCGAAAGTGAAGAAATATG 378
Db 301 TCCACCACAACTGTACACCTGAATTCACAGGCCAATGAAGTTCCGAAAGTGAAGAAATATG 360
QY 379 AACAGGATTCATCACAGACCCCTGTGTCCTCAGCCCCAAGGATCGCGTGGGATGTTT 438
Db 361 AACAGGATTCATCACAGACCCCTGTGTCCTCAGCCCCAAGGATCGCGTGGGATGTTT 420
QY 439 TTGAGGCCAAGGCCCCGGCATGGTTTCTGCGGTATCCCAATCACAGACACAGGCCCGATGG 498
Db 421 TTGAGGCCAAGGCCCCGGCATGGTTTCTGCGGTATCCCAATCACAGACACAGGCCCGATGG 480
QY 499 GGAGCCGCTTGGTGGCATCTCTCTCCAGGGAGACATTTTCTCAAGAGAGGAAC 558
Db 481 GGAGCCGCTTGGTGGCATCTCTCTCCAGGGAGACATTTTCTCAAGAGAGGAAC 540
QY 559 ATGACTGTTTCTTGAAGAGATAATGACAAAGAGGAGACTTGTGTAGCCCCCGCA 618
Db 541 ATGACTGTTTCTTGAAGAGATAATGACAAAGAGGAGACTTGTGTAGCCCCCTGCAG 600
QY 619 GCATCACACTGAAGGAGCAAAATGAATTTCTGACGGCAGCAAGAAGGAAAGTTGCCCA 678
Db 601 GCATCACACTGAAGGAGCAAAATGAATTTCTGACGGCAGCAAGAAGGAAAGTTGCCCA 660
QY 679 TTGTAATGAAGATGATGAGCTTTGTGGCATCATTTGCCCGACAGACACCTGAAGAAGATC 738
Db 661 TTGTAATGAAGATGATGAGCTTTGTGGCATCATTTGCCCGACAGACACCTGAAGAAGATC 720
QY 739 GGGACTACCCACTAGCCCTCCAAGATGCCAAGAAACAGCTGCTGTGGGACGCCATTG 798
Db 721 GGGACTACCCACTAGCCCTCCAAGATGCCAAGAAACAGCTGCTGTGGGACGCCATTG 780
QY 799 GCACTCATGAGATGACAAAGTATAGCGCTGACTTGTCCCGACGGCTGTGTGATGATG 858
Db 781 GCACTCATGAGATGACAAAGTATAGCGCTGACTTGTCCCGACGGCTGTGTGATGATG 840
QY 859 TGGTTTGGACTCTTCCACAGGAAATTCATCTTCCAGATCAATATGATCAAGTACATCA 918
Db 841 TGGTTTGGACTCTTCCACAGGAAATTCATCTTCCAGATCAATATGATCAAGTACATCA 900
QY 919 AAGACAATACCCCTAATCTCCAAGTCATTGGAGCAATGTGTCACTGTGCCACAGCCA 978
Db 901 AAGACAATACCCCTAATCTCCAAGTCATTGGAGCAATGTGTCACTGTGCCACAGCCA 960
QY 979 AGACCTCATTTGATGCAGGTGTGATGCCCTGCGGGTGGGATGGGAAGTGGCTCCATCT 1038
Db 961 AGACCTCATTTGATGCAGGTGTGATGCCCTGCGGGTGGGATGGGAAGTGGCTCCATCT 1020
QY 1039 GCATTATCCAGGAAGTGTGGCTGTGGCGGGGGCCCCAAGCAACACAGTGTACAAAGTGT 1098
Db 1021 GCATTATCCAGGAAGTGTGGCTGTGGCGGGGGCCCCAAGCAACAGTGTACAAAGTGT 1080
QY 1099 ATGATATGCACGGCGCTTTGGTGTTCGGGTCAATTGCTGATGAGGAATCCAAAATGTGG 1158
Db 1081 CAGAGTATGCACGGCGCTTTGGTGTTCGGGTCAATTGCTGATGAGGAATCCAAAATGTGG 1140
QY 1159 GTCATATTCGAAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCTGG 1218
Db 1141 GTCATATTCGAAAGCCTTGGCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCTGG 1200
QY 1219 CTGCCACCACTGAGGCCCCCTGGTGAATCTTCTTTCGATGGGATCCGGCTAAAGAAAT 1278
Db 1201 CTGCCACCACTGAGGCCCCCTGGTGAATCTTCTTTCGATGGGATCCGGCTAAAGAAAT 1260
QY 1279 ATCGCGGTATGGGTTCTCTGATGCCATGGAACAAGCACCCTCAGCAGCCAGAACAGATATT 1338
Db 1261 ATCGCGGTATGGGTTCTCTGATGCCATGGAACAAGCACCCTCAGCAGCCAGAACAGATATT 1320
QY 1339 TCAGTGAAGCTGACAAAAATCAAAGTGGGCCAGGGAGTGTCTGTGCTGTGCAGGACAAAG 1398
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Db 1321 TCAGTGAAGCTGACAAAAATCAAAGTGGGCCAGGGAGTGTCTGTGCTGTGCAGGACAAAG 1380
QY 1399 GGTCAATCCACAAATTTGTCCCTTACCTGATGCTGCGCATCCAAACACTCATGCCAGACA 1458
Db 1381 GGTCAATCCACAAATTTGTCCCTTACCTGATGCTGCGCATCCAAACACTCATGCCAGACA 1440
QY 1459 TTGTTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGAGCTTAAGTTTG 1518
Db 1441 TTGTTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATGTACTCTGGGAGCTTAAGTTTG 1500
QY 1519 AGAAGAGAAGCTTCTCAGCCCCAGGTGGAAGGTGGCGTCCATAGCCTCCATTCGTATGAGA 1578
Db 1501 AGAAGAGAAGCTTCTCAGCCCCAGGTGGAAGGTGGCGTCCATAGCCTCCATTCGTATGAGA 1560
QY 1579 AGCGGCTTTTCTGAAGAGGATCCAGCACACCCTCTCGGTTTTTTTTCATATAAGTTT 1638
Db 1561 AGCGGCTTTTCTGAAGAGGATCCAGCACACCCTCTCGGTTTTTTTTCATATAAGTTT 1620
QY 1639 AGAAGA 1645
Db 1621 AGAAGA 1627

RESULT 2
US-09-822-849A-48
: Sequence 48, Application US/09822849A
: Patent No. US20020045170A1
: GENERAL INFORMATION:
: APPLICANT: Wong, Gordon G.
: APPLICANT: Clark, Hilary
: APPLICANT: Rechtel, Kim
: APPLICANT: Agostino, Michael J.
: APPLICANT: Howes, Steven H.
: APPLICANT: Resnick, Richard J.
: APPLICANT: Gulukota, Kamalakkar
: APPLICANT: Graham, James R.
: APPLICANT: Genetics Institute, Inc.
: TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
: FILE REFERENCE: GIN 6403
: CURRENT APPLICATION NUMBER: US/09/822, 849A
: CURRENT FILING DATE: 2001-09-04
: PRIOR APPLICATION NUMBER: 60/195, 582
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 598
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 48
: LENGTH: 1157
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-822-849A-48

Query Match 69.0%; Score 1141.6; DB 10; Length 1157;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 489 GGCCGGATGGGAGCGCGCTTGGTGGGCATCATCTCTCCAGGACATTTGATTTTCTCAAA 548
Db 1 GGCCGGATGGGAGCGCGCTTGGTGGGCATCATCTCTCCAGGACATTTGATTTTCTCAAA 60
QY 549 GAGGAGAACATGACTGTTTCTTGGAGAAGATATGACAAGAGGGAAGACTTGTGTGTA 608
Db 61 GAGGAGAACATGACTGTTTCTTGGAGAAGATATGACAAGAGGGAAGACTTGTGTGTA 120
QY 609 GCGCCCGCAGCATCACACTGAAGGAGCAAAATGAAATTTCTGACGCGCAGCAAGAGGGA 668
Db 121 GCGCCCTGCAGCATCACACTGAAGGAGCAAAATGAAATTTCTGACGCGCAGCAAGAGGGA 180
QY 669 AAGTTGCCATTGTAATGAAGATGATGAGCTTGTGGCATCATTTGCCGAGACAGACTG 728
Db 181 AAGTTGCCATTGTAATGAAGATGATGAGCTTGTGGCATCATTTGCCGAGACAGACTG 240
QY 729 AAGAAGATCGGGACTACCCACTAGCCTCCAAAGATGCCAAGAAACAGCTGTGTGGG 788
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Db 241 AAGAAGATCGGGACTACCCACTAGCCTCCAAGATGCCAAGAACA
QY 789 GCAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGACTGCTG
Db 301 GCAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGACTGCTG
QY 849 GTGGATGATGCTGTTTGGAGCTCTTCCAGGGAATTCATCTTCCAG
Db 361 GTGGATGATGCTGTTTGGAGCTCTTCCAGGGAATTCATCTTCCAG
QY 909 AAGTACATCAAGAACAATACCCCTAATCTCCAAGTCATTGGAGGCAAT
Db 421 AAGTACATCAAGAACAATACCCCTAATCTCCAAGTCATTGGAGGCAAT
QY 969 GCCCAGGCCAAGAACCCTCATTTGATGCAAGGTGTGGATGCCCTGGCGGTG
Db 481 GCCCAGGCCAAGAACCCTCATTTGATGCAAGGTGTGGATGCCCTGGCGGTG
QY 1029 GGCCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGGGCGGCCCA
Db 541 GGCCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGGGCGGCCCA
QY 1089 TACAAGTGTATGAGTATGCACGGCGCTTTGGTGTTCGGCTCATTTGCT
Db 601 TACAAGTGTATGAGTATGCACGGCGCTTTGGTGTTCGGCTCATTTGCT
QY 1149 CAAATGTGGGTTCATATTGGGAAGCCTTTGGCCCTTGGGGCCTCCACA
Db 661 CAAATGTGGGTTCATATTGGGAAGCCTTTGGCCCTTGGGGCCTCCACA
QY 1209 TCTCTCCTGGCTGCCACCAGCTGAGGCCCTGGTGAATACTTCTTTTCG
Db 721 TCTCTCCTGGCTGCCACCAGCTGAGGCCCTGGTGAATACTTCTTTTCG
QY 1269 CTAAGAATAATATCGCGGTATGGGTCTCTCGATGCCATGACAGACAG
Db 781 CTAAGAATAATATCGCGGTATGGGTCTCTCGATGCCATGACAGACAG
QY 1329 AACAGATATTTCACTGGAAGCTGACAAATCAAAAGTGGCCAGGAGTG
Db 841 AACAGATATTTCACTGGAAGCTGACAAATCAAAAGTGGCCAGGAGTG
QY 1389 CAGCACAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGC
Db 901 CAGCACAAGGGTCAATCCACAATTTGTCCCTTACCTGATTGCTGGC
QY 1449 TGCCAGACATTTGGTGCCAAAGCTTTGACCCCAAGTCCGAGCCATGATG
Db 961 TGCCAGACATTTGGTGCCAAAGCTTTGACCCCAAGTCCGAGCCATGATG
QY 1509 CTTAAGTTTGAGAGAGAGACGTCCTTCAGCCCCAGGTGGAAGGTGGCGTC
Db 1021 CTTAAGTTTGAGAGAGAGACGTCCTTCAGCCCCAGGTGGAAGGTGGCGTC
QY 1569 TCGTATGAGAAGCGGCTTTTCTGAAAAGGGATCCAGCACACCTCCTCG
Db 1081 TCGTATGAGAAGCGGCTTTTCTGAAAAGGGATCCAGCACACCTCCTCG
QY 1629 ATAAAAGTTTAGAAG 1644
Db 1141 ATAAAAGTTTAGAAG 1156

RESULT 3
US-09-880-107-2119
; Sequence 2119, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2119
; LENGTH: 2858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 J05272
US-09-880-107-2119

Query Match 58.1%; Score 960.8; DB 10; Length 2858;
Best Local Similarity 76.1%; Pred. No. 2,1e-290;
Matches 1184; Conservative 0; Mismatches 372; Indels 0; Gaps 0;

QY 37 CTGTGTGGCCATGGCCGACTACCTGATTAAGTGGGGGACAGCTTACGTGCCAGACGAG 96
Db 590 CAGGGCTAGCCATGGCGGACTACCTGATCAGCGGGCACC GGCTACGTGCCGAGAGATG 649
QY 97 GACTCACAGACAGCAGAGCTCTTCACTGCGGAGACGGCCCTCACCTACATGACTTCTCA 156
Db 650 GCCTCACCGCCGACAGCAGCTCTTCCGCCAGCGCCGACGACCTCACCTACAGACTTCTCA 709
QY 157 TTTCTCCCTGGGTACATCGACTTCACTGACAGACAGCAGGTGACCTGACTTCTGTGACCA 216
Db 710 TTTCTCCAGGATTCATAGACTTCAATGACTGATGAGGTGACCTGACCTCAGCCCTGACCC 769
QY 217 AGAAATPACTCTTAAGACCCCACTGGTTTCCTCTCCCATGACACAGTCAACAGAGGCTG 276
Db 770 GGAAGATPACCTTGAAGACGCCACTCATCTCCTCCCCATGACACTGTGACAGAGGCTG 829
QY 277 GGATGGCCATAGCAATGGCGCTTACAGCGCGGTATTTGGCTTCAATCCACCACTGTACAC 336
Db 830 ACATGGCCATTTGCCATGGCTGTGATGGAGGATTTGGGTTCATTACCACTGTGACACC 889
QY 337 CTGAATPCCAGGCCAATGAAGTTCGGAAGTGAAGAATATGAACAGGGATTTCATCACAG 396
Db 890 CAGAGTTCACAGGCCAATGAAGTACGCAAGTCAAGAATTTGAACAGGGCTTCATCACAG 949
QY 397 ACCCTGTGCTCTCAGCCCCCAAGGATCCGCTGCGGATGTGTTTGAAGGCCAAGGCCGCC 456
Db 950 ACCCTGTGCTCTCAGCCCCCAAGGATCCGCTGCGGATGTGTTTGAAGGCCAAGGCGCC 1009
QY 457 ATGCTTCTGCGGTATCCCAATTCACACACAGCGCCGATGGGAGCCGCTTGTGGGCA 516
Db 1010 ATGCTTCTGCGGTATCCCAATTCACACACAGCGCGGATGGGAGCCGCTTGTGGGCA 1069
QY 517 TCATCTCCCTCAGGGACATTTCTCAAGAGAGGAGGACATGACTGTTTCTTGGAG 576
Db 1070 TCCTACCTCCCGAGACATGACTTTCTTGTGAGAGAGGACACACACCCTCTCAGTG 1129
QY 577 AGATATGACAAGAAGAGGAGGAGTGTGTAGCCCCCGGACGATCACACTGAAGAGAG 636
Db 1130 AGGTGATGACGCCCAAGGATTTGAAGTGTGTGGCTCCAGCAGGTGTGACGTTGAAGAGG 1189
QY 637 CAAATGAATTTCTGACGCGCAGCAGCAAGAGGGAAGTTGCCCATTTGAATGAAGATGATG 696
Db 1190 CAAATGAGATCTCTGACGCGTACGCAAGAAAGGAGCTGCCCTATCTGCAATGATTTGCCATG 1249
QY 697 AGCTTTGGCCATCATTTGCCCGCAGACAGCTGAAGAAGAATCGGACTACCCACTAGCCT 756
Db 1250 AGCTTTGGCCATCATTTGCCCGCAGCAGCTGAAGAAGAATCGAAGTACCTCTTGCGCT 1309
QY 757 CCAAGATGCCAAGAAGCAGCTGCTGTGGGGCAGCCATTGGCCTCATGAGGATGACA 816
Db 1310 CCAAGATTTCCAGAGCAGCTGCTGTGGGGCAGCTGTGGGCCACCCGTGAGGATGACA 1369

QY	817	AGTATAGGCTGGACTTTCCTCGCCCAAGGCTGGTGTGGATGTAGTGGTTTGGACTTCTTCCC	876
		1 11 111111 111 111111 11 11 11 11 11 11 111 1111	
Db	1370	AATACCGTCTGGACCTGCTGACCACAGCGGGGGGTGCAGCGTCATAGTCTTCCACTGCTCCC	1429
QY	877	AGGGAATTCATCTTCAGATCAATATGATCAAGTACATCAAGACAATACCTAATC	936
		1 11 1111 1 11111 111 1 11111111 1 111111 1 11111 1 1	
Db	1430	AAGGAATTCGGTGTATCAGATCGCCATGCTGTCATTCATCAAAACAGAAGTACCCACC	1489
QY	937	TCCAAGTCATTGGAGCAATGTGTCACCTGCTGCCAGGCCAAGAACCTCATGTGACG	996
		1111 1 1111 1 11111 1 1111 1 1 111111111111 111111 1	
Db	1490	TCCAGCTGATTGGGGGAGACGTGCTGACAGCAGCCCGCAAGAACCTGATTGATGCTG	1549
QY	997	GTTGTGATGCCCTGCGGTTGGGCATGGGAAGTGGCTCCATCTGCATTATCCAGAAGTGC	1056
		111111 1 1111 1111111111 1 11111111111 1 111111111	
Db	1550	GTTGTGACGGGCTCGCGGTGGGCATGGGCTCGCGGCTCCATCTGCATCACCCAGAAGTGA	1609
QY	1057	TGGCCTGTGGGCGGCCCAAGCAACAGCAGTGTACAAAGTGTATGAGTATGCAGCGGCT	1116
		111111111 1111111 1 11 11111111111 1111111 1111111	
Db	1610	TGGCCTGTGTTGGGCCCCCAGGGCACCTGCTGTGTACAAAGTGGCTGAGTATGCCCGGCT	1669
QY	1117	TTGGTGTTCCGGTCATGTCTGATGGAGGAATCCAAATGTGGGTCTATATTGCCAAAGCCT	1176
		111111 11 1111 11 1111 11 1111 1 1111 1 1 11 11 111	
Db	1670	TTGGTGTGCCCATCATAGCCGATGGCGGCATCCAGACCGTGGGACACAGTGGTCAAGGCC	1729
QY	1177	TGGCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCTGCTGCCACCACTGAGGCC	1236
		11111111 11111111 11111111 11111111 11 11111 11 11111	
Db	1730	TGGCCTTGGAGCCTCCACAGTGTATGATGGGCTCCCTGCTGGCCGCCACTACGAGGCC	1789
QY	1237	CTGGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATATCGCGTATGGGTCTC	1296
		1111 11 111111 11 11 11 11 11 11 11 11 11 11 11 11 11 11	
Db	1790	CTGGCGAGTACTTCTTCTCAGACGGGGTCCGGCTCAAGAAGTACCGGGCATGGCGCTCAC	1849
QY	1297	TGCATGCCATGGACAAGCACCTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAATA	1356
		1 111 111111 111 1 1111111111 111 1111 11 1 1111	
Db	1850	TGGATCCCATGGAGAAGAGCAGCAGCAGCAGAAACGATCTTCAGCGAGGGGATAAAG	1909
QY	1357	TCAAGTGGCCCCAGGAGTGTCTGTGCTGTGCAGGACAAAGGGTCAATCCACAATTTG	1416
		1 11 1 11 1111 11 11 1 1 1 11111111 11 11 11 11 11 1	
Db	1910	TGAAGATCGCACAGGGTGTCTCGGGCTCCATCCAGGACAAAGATTCATTCAGAAAGTTG	1969
QY	1417	TCCCTTACCTGATGTGCTGGCATCCAACTCATCTATGCCAGGACATTTGGTCCCAAGACTTGA	1476
		1 11 1111 11 11 1111111111 1111111 11 1111 11 11 11	
Db	1970	TGCCCTACCTCATAGCAGGACATCCAACACGGCTGCCAGGATATCGGGGCCGAGCCTGT	2029
QY	1477	CCCAAGTCCGAGCATGATGTACTCTGGGAGCTTAAGTTGAGAAGAGAACGTCTCAG	1536
		1 11 11 1111111111 11 1111 1111111111 11 11	
Db	2030	CTGTCTTTCGGTCCATGATGTACTCAGAGAGCTCAAGTTTGAGAAAGCGACCATGTGCG	2089
QY	1537	CCGAGGTGAAGGTGGCGTCCATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA	1592
		11111 1 11 1111 11111 111 11 11 11 111111 1 1111	
Db	2090	CCGAGATTGAGGGTGGTGTCCATGGCCCTGCACCTTACGAAAAAGCGGCTGTACTGA	2145
RESULT 4			
US-09-853-918-45			
: Sequence 45, Application US/09853918			
: Patent NO. US20020068346A1			
: GENERAL INFORMATION:			
: APPLICANT: Krystek, Stanley R.			
: APPLICANT: Sheriff, Steven			
: APPLICANT: Wilmer, Mark R.			
: APPLICANT: Hollenbaugh, Diane L.			
: APPLICANT: Yan, Ning			
: APPLICANT: Mouravieff, Julie E.			
: APPLICANT: Einspahr, Howard M.			
: APPLICANT: Kish, Kevin			
: TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE			
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF			
: FILE REFERENCE: DB24NP			
: CURRENT APPLICATION NUMBER: US/09/853,918			
: CURRENT FILING DATE: 2001-05-10			
: PRIOR APPLICATION NUMBER: 60/203,448			
: PRIOR FILING DATE: 2000-05-10			

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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-853-918-45

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Query Match	49.4%;	Score 816.4;	DB 10;	Length 1158;
Best Local Similarity	98.7%;	pred. No. 2.1e-245;		
Matches 823; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0

QY	759	AAAGATGCCAAGAAACAGCTGCTGTGTGGGGCAGCCATTGGCAGCTCATGAGGATGACAAG	818
Db	325	AAATATTCTCCGACTCAGCTGTGTGTGGGGCAGCCATTGGCAGCTCATGAGGATGACAAG	384
QY	819	TATAGGCTGGACTTGCTGCGCCCAAGGCTGCTGTGTGGATGATGCTGTTTGGAGCTCTTCCAG	878
Db	385	TATAGGCTGGACTTGCTGCGCCCAAGGCTGCTGTGTGGATGATGCTGTTTGGAGCTCTTCCAG	444
QY	879	GGAATTTCCATCTTCCAGATCAATATGATCAAGTACATCAAGAACAATATACCCTAATCTC	938
Db	445	GGAATTTCCATCTTCCAGATCAATATGATCAAGTACATCAAGAACAATATACCCTAATCTC	504
QY	939	CAAGTCATTGGAGGCCAATGTGTCACTGCTGCCCCAGGCCCCAAGAACCTCATTTGATGCAGT	998
Db	505	CAAGTCATTGGAGGCCAATGTGTCACTGCTGCCCCAGGCCCCAAGAACCTCATTTGATGCAGT	564
QY	999	GTEGATGCCCTGCGGGGTGGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTG	1058
Db	565	GTEGATGCCCTGCGGGGTGGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTG	624
QY	1059	GCCGTGTGGGGCCCCCAAGCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCGCTTT	1118
Db	625	GCCGTGTGGGGCCCCCAAGCAACAGCAGTGTACAAAGTGTATGAGTATGCACGGCGCTTT	684
QY	1119	GGTGTTCGGGTCAATTGCTGATGAGGAATCCAAAATGTGGGTCAATATTGGCAAAAGCTTG	1178
Db	685	GGTGTTCGGGTCAATTGCTGATGAGGAATCCAAAATGTGGGTCAATATTGGCAAAAGCTTG	744
QY	1179	GCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCGCTGCCCCACACAGTGAAGGCCCT	1238
Db	745	GCCCTTGGGGCCTCCACAGTCATGATGGGCTCTCTCGCTGCCCCACACAGTGAAGGCCCT	804
QY	1239	GGTGAATACTTCTTTTCCGATGGGATCCGGCTAAAGAATAATCCGGGTATGGGTTCTCTC	1298
Db	805	GGTGAATACTTCTTTTCCGATGGGATCCGGCTAAAGAATAATCCGGGTATGGGTTCTCTC	864
QY	1299	GATGCCATGGACAAGCACCTTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAAATC	1358
Db	865	GATGCCATGGACAAGCACCTTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAAATC	924
QY	1359	AAAGTGGCCAGGGAGTGTCTGTGCTGTGACAGGACAAAGGCTCAATCCACAAATTTGTC	1418
Db	925	AAAGTGGCCAGGGAGTGTCTGTGCTGTGACAGGACAAAGGCTCAATCCACAAATTTGTC	984
QY	1419	CCTTACCTGATTTGCTGGCATCCAACACTCATGACCAGGACATTGGTCCAAAGAGCTTGACC	1478
Db	985	CCTTACCTGATTTGCTGGCATCCAACACTCATGACCAGGACATTGGTCCAAAGAGCTTGACC	1044
QY	1479	CAAGTCCGAGCCATGATGTACTCTGGGGAGCTTAAGTTTGAGAGAAGAGCTCCTCAGCC	1538
Db	1045	CAAGTCCGAGCCATGATGTACTCTGGGGAGCTTAAGTTTGAGAGAAGAGCTCCTCAGCC	1104
QY	1539	CAGGTGGAAGGTGGCGTCCATAGCCTCCATTGCTATGAGAAGCGGCTTTTCTGA	1592
Db	1105	CAGGTGGAAGGTGGCGTCCATAGCCTCCATTGCTATGAGAAGCGGCTTTTCTGA	1158

RESULT 5
US-09-853-918-46
; Sequence 46, Application US/09853918
; Patent No. US20020068346A1


```

: GENERAL INFORMATION:
: APPLICANT: Krystek, Stanley R.
: APPLICANT: Sheriff, Steven
: APPLICANT: Wilmer, Mark R.
: APPLICANT: Hollenbaugh, Diane L.
: APPLICANT: Yan, Ning
: APPLICANT: Mouravieff, Julie E.
: APPLICANT: Einspahr, Howard M.
: APPLICANT: Kish, Kevin
: TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
: TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
: FILE REFERENCE: DB24NP
: CURRENT APPLICATION NUMBER: US/09/853,918
: CURRENT FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: 60/203,448
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 46
: LENGTH: 1158
: TYPE: DNA
: ORGANISM: Homo sapiens
US-853-918-46

```

Query Match	49.28;	Score 813.2;	DB 10;	Length 1158;
Best Local Similarity	98.48;	Pred. No. 2.1e-244;		
Matches 821;	Conservative	0;	Mismatches 13;	Indels 0;
				Gaps 0;

QY	759	AAAGATGCCAAGAAACAGCTGCTGTGTGGGGCAGCCATTGGCACTCAT	AGAGTATACAAG	818
Db	325	AAATATGCTGGTCGTCCGCTGCTGTGTGGGGCAGCCATTGGCACTCAT	AGAGTATACAAG	384
QY	819	TATAGGCTGGACTTGCCTGCCCGCAGGCTGGTGTGATGTAGTGGTTTG	ACTCTTCCAG	878
Db	385	TATAGGCTGGACTTGCCTGCCCGCAGGCTGGTGTGATGTAGTGGTTTG	ACTCTTCCAG	444
QY	879	GGAATTTCCATCTTCCAGATCAATATATGATCAAGTACATCAAGACAAA	ACCCTTAATCTC	938
Db	445	GGAATTTCCATCTTCCAGATCAATATATGATCAAGTACATCAAGACAAA	ACCCTTAATCTC	504
QY	939	CAAGTCATTGGAGGCAATGTGTCACCTGCTGCCCGCAGCCAAAGAACCTC	TTTGATGCAGT	998
Db	505	CAAGTCATTGGAGGCAATGTGTCACCTGCTGCCCGCAGCCAAAGAACCTC	TTTGATGCAGT	564
QY	999	GTGATGCCCTGCGGGTGGGCATGGGAAGTGGCTTCATCTGCATTATC	AGGAAGTGCTG	1058
Db	565	GTGATGCCCTGCGGGTGGGCATGGGAAGTGGCTTCATCTGCATTATC	AGGAAGTGCTG	624
QY	1059	GCCTGTGGGGCGGCCCAAGCAACAGCAGTGTACAACTGTATGAGTATC	CACGGCGCTTT	1118
Db	625	GCCTGTGGGGCGGCCCAAGCAACAGCAGTGTACAACTGTATGAGTATC	CACGGCGCTTT	684
QY	1119	GGTGTCCCGGTCAATTGCTGATGGAGGAATCCAAATGTGGGTCAATATTC	CCGAAGCCTTG	1178
Db	685	GGTGTCCCGGTCAATTGCTGATGGAGGAATCCAAATGTGGGTCAATATTC	CCGAAGCCTTG	744
QY	1179	GGCCTTGGGGCGCTCCACAGTCATGATGGGCTCTCTCTGGCTGCCACC	CTGAGGCCCTT	1238
Db	745	GGCCTTGGGGCGCTCCACAGTCATGATGGGCTCTCTCTGGCTGCCACC	CTGAGGCCCTT	804
QY	1239	GGTGAATACCTTCTTTCCGATGGGATCCGGCTTAAGAAATATCGCGGT	ATGGGTTCTCTC	1298
Db	805	GGTGAATACCTTCTTTCCGATGGGATCCGGCTTAAGAAATATCGCGGT	ATGGGTTCTCTC	864
QY	1299	GATGCCATGGACAACACCTCAGCAGCCAGAACACATATTTCACTGAAC	CTGACAAAATC	1358
Db	865	GATGCCATGGACAACACCTCAGCAGCCAGAACACATATTTCACTGAAC	CTGACAAAATC	924
QY	1359	AAAGTGGCCCAAGGAGTGTCTGTGTGTGTGCAGAGCAAAAGGGTCAATC	ACAAAATTTGTC	1418
Db	925	AAAGTGGCCCAAGGAGTGTCTGTGTGTGTGCAGAGCAAAAGGGTCAATC	ACAAAATTTGTC	984
QY	1419	CCTTACCTGATTTGCTGGCATCCAACACTCATGTCCAGAGCATTTGGTGCCA	AGAGCTTGACC	1478

D _b	985	CCTTACCTGATTTGGTCGCATCCAACACTCATTGCCAGACAATTGGTGCCAAAGAGCCTTAGACC	1044
QY	1479	CAAGTCCGAGCCATGATGTACTCTGGGGAGCCTTAAGTTTGAGAAGAGAACGTCCTCACGCC	1538
D _b	1045	CAAGTCGAGCCATGATGTACTCTGGGGAGCCTTAAGTTTGAGAAGAGAACGTCCTCACGCC	1104
QY	1539	CAGGTGAAGCGTGGCGTTCATAGCCCTCCATTTCGTATGACAAGCGGCTTTTCTGA	1592
D _b	1105	CAGGTGAAGGTGGCGTTCATAGCCCTCCATTTCGTATGACAAGCGGCTTTTCTGA	1158

```

RESULT 6
US-09-853-918-47
; Sequence 47, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-853-918-47

```

Query Match	49.0%;	Score 810;	DB 10;	Length 1158;	
Best Local Similarity	98.2%;	Pred. No. 2.1e-243;			
Matches 819;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;	
QY 759	AAAGATGCCAAGAAACAGCTGCTGTGTGGGCGACCCATTGGCACTCATGAGATGACAAG	818			
Db 325	AAATATAACTCTCCGCTTCTGCTGTGTGGGCGACCCATTGGCACTCATGAGATGACAAG	384			
QY 819	TATAGGCTGGACCTGCTCGGCCAGGCTGCTGTGGATGATAGTGTGTTGGACCTCTTCCAG	878			
Db 385	TATAGGCTGGACCTGCTCGGCCAGGCTGCTGTGGATGATAGTGTGTTGGACCTCTTCCAG	444			
QY 879	GGAATTCATCTTCCAGATCATATGATCAAGTACATCAAGAACAATACCCCTAATCTC	938			
Db 445	GGAATTCATCTTCCAGATCATATGATCAAGTACATCAAGAACAATACCCCTAATCTC	504			
QY 939	CAAGTCATTGGAGGCAATGTGGTCACTGCTGCCAGGCCAAGAACCTCATTTGATGCAGGT	998			
Db 505	CAAGTCATTGGAGGCAATGTGGTCACTGCTGCCAGGCCAAGAACCTCATTTGATGCAGGT	564			
QY 999	GTGGATGCCCTCGGGGTGGGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGCTG	1058			
Db 565	GTGGATGCCCTCGGGGTGGGCATGGGAAGTGGCTCCATCTGCATTTATCCAGGAAGTGCTG	624			
QY 1059	GCCTGTGGGGCCCCCAAGCAACAGCAGTGTACAAAGGTGTATGAGTATGCACGGCGCTTT	1118			
Db 625	GCCTGTGGGGCCCCCAAGCAACAGCAGTGTACAAAGGTGTACAGAGTATGCACGGCGCTTT	684			
QY 1119	GGTGTTCGGGTCAATTGCTGATGGAGGAATCCAAAAATGTGGGTCAATTTGGCAAAGCCTTG	1178			
Db 685	GGTGTTCGGGTCAATTGCTGATGGAGGAATCCAAAAATGTGGGTCAATTTGGCAAAGCCTTG	744			
QY 1179	GCCCTTGGGGCTCCACAGTCATGATGGGCTCTCTCTGCGTGCACCACTGAGGCGCCCT	1238			

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|||||
Db 745 GGCCTTGGGCGCTCACAGTCATGATGGGCTCTGCTGGCTGCCACCACTGAGGCCCT 804

QY 1239 GGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATATCCGGTATGGGTTCTCTC 1298
|||||
Db 805 GGTGAATACTTCTTTCCGATGGGATCCGGCTAAAGAAATATCCGGTATGGGTTCTCTC 864

QY 1299 GATGCCATGGACAAGCACTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAATC 1358
|||||
Db 865 GATGCCATGGACAAGCACTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAATC 924

QY 1359 AAAGTGGCCAGGAGTGTCTGTGCTGTGCAGGACAAAGGTCATCCACAATTTGTC 1418
|||||
Db 925 AAAGTGGCCAGGAGTGTCTGTGCTGTGCAGGACAAAGGTCATCCACAATTTGTC 984

QY 1419 CCTTACCTGATTGCTGGCATCCAACTCATGCGCAGACATTGGTCCAGAGCTTGACC 1478
|||||
Db 985 CCTTACCTGATTGCTGGCATCCAACTCATGCGCAGACATTGGTCCAGAGCTTGACC 1044

QY 1479 CAAGTCCGAGCCATGATGTACTCTGGGAGCTTAAAGTTGAGAAAGAAACGTCCTCAGCC 1538
|||||
Db 1045 CAAGTCCGAGCCATGATGTACTCTGGGAGCTTAAAGTTGAGAAAGAAACGTCCTCAGCC 1104

QY 1539 CAGGTGGAAGTGGCGCTCCATAGCCTCCATTGCTATGAGAAGCGGCTTTCTGA 1592
|||||
Db 1105 CAGGTGGAAGTGGCGCTCCATAGCCTCCATTGCTATGAGAAGCGGCTTTCTGA 1158
```

```
RESULT 7
US-09-853-918-40
; Sequence 40, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Wilmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-853-918-40
```

```
Query Match 48.9%; Score 809.6; DB 10; Length 1155;
Best Local Similarity 99.5%; Pred. No. 2.8e-243;
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 777 CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGGATGACAAGTATAGGCTGGACTTGCTC 836
|||||
Db 340 CTGCTGTGTGGGCGAGCCATTGGCACTCATGAGGATGACAAGTATAGGCTGGACTTGCTC 399

QY 837 GCCCAGGCTGTGTGATGTAGTGTGTTGGACTCTTCCAGGGAATTCATCTTCCAG 896
|||||
Db 400 GCCCAGGCTGTGTGATGTAGTGTGTTGGACTCTTCCAGGGAATTCATCTTCCAG 459

QY 897 ATCAATATGATCAAGTACATCAAAAGCAAAATACCCTAATCTCCAAGTCATTGGAGCAAT 956
|||||
Db 460 ATCAATATGATCAAGTACATCAAAAGCAAAATACCCTAATCTCCAAGTCATTGGAGCAAT 519

QY 957 GTGCTACTGCTGCCAGGCCAAGAACTCATTTGATGCAGGTTGTGATGCCCTGCGGCTG 1016
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|||||
Db 520 GTGCTACTGCTGCCAGGCCAAGAACTCATTTGATGCAGGTGTGATGCCCTGCGGCTG 579

QY 1017 GGCATGGGAAGTGCTCCATCTGCATTATCCAGGAAGTGCTGGCCGTGGCGGCCCA 1076
|||||
Db 580 GGCATGGGAAGTGCTCCATCTGCATTATCCAGGAAGTGCTGGCCGTGGCGGCCCA 639

QY 1077 GCAACAGCAGTGTACAGGTGTATGAGTATGCACGGCGCTTTGGTGTCCGTCATTGCT 1136
|||||
Db 640 GCAACAGCAGTGTACAGGTGTACAGTATGCACGGCGCTTTGGTGTCCGTCATTGCT 699

QY 1137 GATGGAGGAATCCAAATGTGGGTCAATATTCGAAAGCCTTGGCCCTTGGGCGCTCCACA 1196
|||||
Db 700 GATGGAGGAATCCAAATGTGGGTCAATATTCGAAAGCCTTGGCCCTTGGGCGCTCCACA 759

QY 1197 GTCATGATGGGCTCTCTCTCTGGCTGCCACCACCTGAGGCCCTGGTGAATACTTCTTCC 1256
|||||
Db 760 GTCATGATGGGCTCTCTCTCTGGCTGCCACCACCTGAGGCCCTGGTGAATACTTCTTCC 819

QY 1257 GATGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCGATGCCATGACAGCAC 1316
|||||
Db 820 GATGGATCCGGCTAAAGAAATATCGCGGTATGGGTTCTCGATGCCATGACAGCAC 879

QY 1317 CTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAATCAAAAGTGCCAGGGAGTG 1376
|||||
Db 880 CTCAGCAGCCAGAACAGATATTTCAGTGAAGCTGACAAATCAAAAGTGCCAGGGAGTG 939

QY 1377 TCTGTGCTGTGCAGAGCAAGGGTCAATCCACAATTTGTCCCTTACCTGATGCTGGC 1436
|||||
Db 940 TCTGTGCTGTGCAGAGCAAGGGTCAATCCACAATTTGTCCCTTACCTGATGCTGGC 999

QY 1437 ATCCAACACTCATGCGCAGACATTTGGTGCCAAGAGCTTGACCCAAAGTCCGAGCCATGATG 1496
|||||
Db 1000 ATCCAACACTCATGCGCAGACATTTGGTGCCAAGAGCTTGACCCAAAGTCCGAGCCATGATG 1059

QY 1497 TACTCTGGGAGCTTAAGTTTGAGAAGAGAAGCAAGCTCTCAGCCAGGTGGAAGTGCGCTC 1556
|||||
Db 1060 TACTCTGGGAGCTTAAGTTTGAGAAGAGAAGCAAGCTCTCAGCCAGGTGGAAGTGCGCTC 1119

QY 1557 CATAGCCTCCATTGCTATGAGAAGCGGCTTTCTGA 1592
|||||
Db 1120 CATAGCCTCCATTGCTATGAGAAGCGGCTTTCTGA 1155
```

```
RESULT 8
US-09-853-918-41
; Sequence 41, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Wilmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-853-918-41
```

```
Query Match 48.9%; Score 809.6; DB 10; Length 1155;
```

Best Local Similarity 99.5%; Pred. No. 2.8e-243;
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	777	CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGCCTGGACTTGCTC	836
Db	340	CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGCCTGGACTTGCTC	399
QY	837	GCCGAGGCTGCTGTGATGTAGTGTGCTTTGGACTCTTCCAGGGAATTCATCTTCCAG	896
Db	400	GCCGAGGCTGCTGTGATGTAGTGTGCTTTGGACTCTTCCAGGGAATTCATCTTCCAG	459
QY	897	ATCAATATGATCAAGTACATCAAGACAATAATACCCTAATCTCCAGTCAATTGGAGGCAAT	956
Db	460	ATCAATATGATCAAGTACATCAAGACAATAATACCCTAATCTCCAGTCAATTGGAGGCAAT	519
QY	957	GTGTCACTGCTGCCCCAGGCCAAGACCTCATTTGATGACAGTGTGATGCCCTGGGGTG	1016
Db	520	GTGTCACTGCTGCCCCAGGCCAAGACCTCATTTGATGACAGTGTGATGCCCTGGGGTG	579
QY	1017	GCCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGGGGCCCCAA	1076
Db	580	GCCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGGGGCCCCAA	639
QY	1077	GCAACAGCAGTGTACAAGGTGTATGATATGCACGCGCGCTTTGGTGTCCGGTCATTGCT	1136
Db	640	GCAACAGCAGTGTACAAGGTGTATGATATGCACGCGCGCTTTGGTGTCCGGTCATTGCT	699
QY	1137	GATGAGGAATCCAAAATGTGGGTCAATTTGCCGAAGCCCTTGCCCTTGCGGCTCCACA	1196
Db	700	GATGAGGAATCCAAAATGTGGGTCAATTTGCCGAAGCCCTTGCCCTTGCGGCTCCACA	759
QY	1197	GTCTATGATGGCTCTCTCTCGCTGGCTGCCACCACCTGAGGCCCTGGTGAACTCTTTTCC	1256
Db	760	GTCTATGATGGCTCTCTCTCGCTGGCTGCCACCACCTGAGGCCCTGGTGAACTCTTTTCC	819
QY	1257	GATGGATCCCGCTAAAGAAATATCGCGGTATGGTCTCTCGATGCCATGACAAGCAC	1316
Db	820	GATGGATCCCGCTAAAGAAATATCGCGGTATGGTCTCTCGATGCCATGACAAGCAC	879
QY	1317	CTCAGCAGCCAGAACAGATATTTCACTGAAGCTGACAAAATCAAAGTGCCCCAGGAGTG	1376
Db	880	CTCAGCAGCCAGAACAGATATTTCACTGAAGCTGACAAAATCAAAGTGCCCCAGGAGTG	939
QY	1377	TCGTGCTGTGTCAGGACAAGGGTCAATCCACAATTTGCTCCCTTACCTGATTGCTGGC	1436
Db	940	TCGTGCTGTGTCAGGACAAGGGTCAATCCACAATTTGCTCCCTTACCTGATTGCTGGC	999
QY	1437	ATCCACACTCATGTCAGGACCATTTGTCACAAGAGCTTGACCCAAGTCGAGCCATGATG	1496
Db	1000	ATCCACACTCATGTCAGGACCATTTGTCACAAGAGCTTGACCCAAGTCGAGCCATGATG	1059
QY	1497	TACTCTGGGGAGCTTAAGTTTGAGAAGAAAGTCTCTCAGCCAGGCTGAAGGTGGCGTC	1556
Db	1060	TACTCTGGGGAGCTTAAGTTTGAGAAGAAAGTCTCTCAGCCAGGCTGAAGGTGGCGTC	1119
QY	1557	CATAGCCTCCATTCTGTATGAGAAGCGGCTTTTCTGA	1592
Db	1120	CATAGCCTCCATTCTGTATGAGAAGCGGCTTTTCTGA	1155

RESULT 9
US-09-853-918-42
; Sequence 42, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Wilmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin

TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; PRIOR FILING DATE: 2001-05-10
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-853-918-42

Query Match 48.9%; Score 809.6; DB 10; Length 1155;
Best Local Similarity 99.5%; Pred. No. 2.8e-243;
Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	777	CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGCTC	836
Db	340	CTGCTGTGTGGGGCAGCCATTGGCACTCATGAGATGACAAGTATAGGCTGGACTTGCTC	399
QY	837	GCCGAGGCTGCTGTGATGTAGTGTGCTTTGGACTCTTCCAGGGAATTCATCTTCCAG	896
Db	400	GCCGAGGCTGCTGTGATGTAGTGTGCTTTGGACTCTTCCAGGGAATTCATCTTCCAG	459
QY	897	ATCAATATGATCAAGTACATCAAGACAATAATACCCTAATCTCCAGTCAATTGGAGGCAAT	956
Db	460	ATCAATATGATCAAGTACATCAAGACAATAATACCCTAATCTCCAGTCAATTGGAGGCAAT	519
QY	957	GTGTCACTGCTGCCCCAGGCCAAGACCTCATTTGATGACAGTGTGATGCCCTGGGGTG	1016
Db	520	GTGTCACTGCTGCCCCAGGCCAAGACCTCATTTGATGACAGTGTGATGCCCTGGGGTG	579
QY	1017	GCCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGGGGCCCCAA	1076
Db	580	GCCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGGGGCCCCAA	639
QY	1077	GCAACAGCAGTGTACAAGGTGTATGATATGCACGCGCGCTTTGGTGTCCGGTCATTGCT	1136
Db	640	GCAACAGCAGTGTACAAGGTGTATGATATGCACGCGCGCTTTGGTGTCCGGTCATTGCT	699
QY	1137	GATGAGGAATCCAAAATGTGGGTCAATTTGCCGAAGCCCTTGCGGCTCCACA	1196
Db	700	GATGAGGAATCCAAAATGTGGGTCAATTTGCCGAAGCCCTTGCGGCTCCACA	759
QY	1197	GTCTATGATGGCTCTCTCTCGCTGGCTGCCACCACCTGAGGCCCTGGTGAATACTTCTTTC	1256
Db	760	GTCTATGATGGCTCTCTCTCGCTGGCTGCCACCACCTGAGGCCCTGGTGAATACTTCTTTC	819
QY	1257	GATGGATCCCGCTAAAGAAATATCGCGGTATGGTCTCTCGATGCCATGACAAGCAC	1316
Db	820	GATGGATCCCGCTAAAGAAATATCGCGGTATGGTCTCTCGATGCCATGACAAGCAC	879
QY	1317	CTCAGCAGCCAGAACAGATATTTCACTGAAGCTGACAAAATCAAAGTGCCCCAGGAGTG	1376
Db	880	CTCAGCAGCCAGAACAGATATTTCACTGAAGCTGACAAAATCAAAGTGCCCCAGGAGTG	939
QY	1377	TCGTGCTGTGTCAGGACAAGGGTCAATCCACAATTTGCTCCCTTACCTGATTGCTGGC	1436
Db	940	TCGTGCTGTGTCAGGACAAGGGTCAATCCACAATTTGCTCCCTTACCTGATTGCTGGC	999
QY	1437	ATCCACACTCATGTCAGGACCATTTGTCACAAGAGCTTGACCCAAGTCGAGCCATGATG	1496
Db	1000	ATCCACACTCATGTCAGGACCATTTGTCACAAGAGCTTGACCCAAGTCGAGCCATGATG	1059
QY	1497	TACTCTGGGGAGCTTAAGTTTGAGAAGAAAGTCTCTCAGCCAGGCTGAAGGTGGCGTC	1556
Db	1060	TACTCTGGGGAGCTTAAGTTTGAGAAGAAAGTCTCTCAGCCAGGCTGAAGGTGGCGTC	1119
QY	1557	CATAGCCTCCATTCTGTATGAGAAGCGGCTTTTCTGA	1592

Db 1120 CATAGCCTCCATTCGTATGAGAGCGGCTTTCTGA 1155

RESULT 10

US-09-853-918-43

; Sequence 43, Application US/09853918

; Patent No. US20020068346A1

; GENERAL INFORMATION:

; APPLICANT: Krystek, Stanley R.

; APPLICANT: Sheriff, Steven

; APPLICANT: Wilmer, Mark R.

; APPLICANT: Hollenbaugh, Diane L.

; APPLICANT: Yan, Ning

; APPLICANT: Mouravieff, Julie E.

; APPLICANT: Einspahr, Howard M.

; APPLICANT: Kish, Kevin

; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE

; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF

; FILE REFERENCE: DB24NP

; CURRENT APPLICATION NUMBER: US/09/853,918

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 60/203,448

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 43

; LENGTH: 1155

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-853-918-43

Query Match 48.9%; Score 809.6; DB 10; Length 1155;

Best Local Similarity 99.5%; Pred. No. 2.8e-243;

Matches 812; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 777 CTGCTGTGGGGCAGCCATTGGCACTCATGAGGATGACAAGTATAGGCTGGACTTGCTC 836

|||||

Db 340 CTGCTGTGGGGCAGCCATTGGCACTCATGAGGATGACAAGTATAGGCTGGACTTGCTC 399

QY 837 GCCAGGCTGGTGTGATGTAGTGTGGACTCTTCCAGGGAATTTCCATCTTCCAG 896

|||||

Db 400 GCCAGGCTGGTGTGATGTAGTGTGGACTCTTCCAGGGAATTTCCATCTTCCAG 459

QY 897 ATCAATATGATCAAGTACATCAAGACAATAACCTAATCTCCAAGTCATTGGAGGCAAT 956

|||||

Db 460 ATCAATATGATCAAGTACATCAAGACAATAACCTAATCTCCAAGTCATTGGAGGCAAT 519

QY 957 GTGCTACTGCTGCCAGGCCAAGACCTCATTTGATGCAGGTGTGGATGCCCTGGCGGTG 1016

|||||

Db 520 GTGCTACTGCTGCCAGGCCAAGACCTCATTTGATGCAGGTGTGGATGCCCTGGCGGTG 579

QY 1017 GGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGCGGCCCAA 1076

|||||

Db 580 GGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGGCTGTGGCGGCCCAA 639

QY 1077 GCAACAGCAGTGTACAAGGTGTATGAGTATGCACGGCGCTTGTGTTCCGGTCATTGCT 1136

|||||

Db 640 GCAACAGCAGTGTACAAGGTGTACAGATATGCACGGCGCTTGTGTTCCGGTCATTGCT 699

QY 1137 GATGAGGAATCCAAAATGTGGGTCTATTTGCGAAAAGCCTTGCCCTTGCGGCTCCACA 1196

|||||

Db 700 GATGAGGAATCCAAAATGTGGGTCTATTTGCGAAAAGCCTTGCCCTTGCGGCTCCACA 759

QY 1197 GTCATGATGGGCTCTCTCTGGCTGCCAACCACTGAGGCCCTGTGAATACTTCTTTCC 1256

|||||

Db 760 GTCATGATGGGCTCTCTCTGGCTGCCAACCACTGAGGCCCTGTGAATACTTCTTTCC 819

QY 1257 GATGGATCCGGCTAAAGAAATATCCGGGTATGGGTCTCTCGATGCCATGGACAAGCAC 1316

|||||

Db 820 GATGGATCCGGCTAAAGAAATATCCGGGTATGGGTCTCTCGATGCCATGGACAAGCAC 879

QY 1317 CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGCACAAAATCAAAAGTGGCCCGAGGAGTG 1376

|||||

Db 880 CTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAAAATCAAAAGTGGCCCGAGGTG 939

QY 1377 TCTGTGCTGTGCAGAGCAAAAGGTCATCCACAAATTTGCCCTTACCTGATTTGCTGGC 1436

|||||

Db 940 TCTGTGCTGTGCAGAGCAAAAGGTCATCCACAAATTTGCCCTTACCTGATTTGCTGGC 999

QY 1437 ATCCAACACTCATGCGCAGACATTTGGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATG 1496

|||||

Db 1000 ATCCAACACTCATGCGCAGACATTTGGTGCCAAGAGCTTGACCCCAAGTCCGAGCCATGATG 1059

QY 1497 TACTCTGGGAGCTTAAGTTTGAGAGAGAACGTCCTCAGCCCAAGGTGGAAGTGGCGTC 1556

|||||

Db 1060 TACTCTGGGAGCTTAAGTTTGAGAGAGAACGTCCTCAGCCCAAGGTGGAAGTGGCGTC 1119

QY 1557 CATAGCCTCCATTCGTATGAGAGCGGCTTTCTGA 1592

|||||

Db 1120 CATAGCCTCCATTCGTATGAGAGCGGCTTTCTGA 1155

RESULT 11

US-10-044-090-65

; Sequence 65, Application US/10044090

; Patent No. US20020137081A1

; GENERAL INFORMATION:

; APPLICANT: Olga Bandman

; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

; FILE REFERENCE: PA-0028 US

; CURRENT APPLICATION NUMBER: US/10/044,090

; CURRENT FILING DATE: 2002-01-09

; NUMBER OF SEQ ID NOS: 850

; SOFTWARE: PERL Program

; SEQ ID NO 65

; LENGTH: 1851

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20020137081A1 1097124.19

US-10-044-090-65

Query Match 39.6%; Score 655.4; DB 12; Length 1851;

Best Local Similarity 84.2%; Pred. No. 8.5e-195;

Matches 839; Conservative 0; Mismatches 11; Indels 147; Gaps 3;

QY 370 AGAATATGAACAGGAGTTCATCACAGACCCTGTGTCTCAGCCCCCAAGATCGCGTGC 429

|||||

Db 855 AGAATATGAACAGGAGTTCATCACAGACCCTGTGTCTCAGCCCCCAAGATCGCGTGC 914

QY 430 GGGATGTTTTGAGGCCAAGCGCCGCGATGTTCTGCGGTATCCCAATCACAGACAG 489

|||||

Db 915 GGGATGTTTTGAGGCCAAGCGCCGCGATGTTCTGCGGTATCCCAATCACAGACAG 974

QY 490 GCCGATGGGAGCGCTGTGGGCATCATCTCCACAGGACATTTGATTTCTCAAAG 549

|||||

Db 975 GCCGATGGGAGCGCGCTGTGGGCATCATCTCCACAGGACATTTGATTTCTCAAAG 1034

QY 550 AGAGGAACATGACTGTTCTTGGAAGAGATTAATGACAAAGAGGAAAGACTTGTGTAG 609

|||||

Db 1035 AGAGGAACATGACTGTTCTTGGAAGAGATTAATGACAAAGAGGAAAGACTTGTGTAG 1094

QY 610 CCCCCGAGCATCACACTGAAGAGGCAATGAATTTCTGAGCCGACGACAAGAG---- 665

|||||

Db 1095 CCCCCGAGGCACTCACACTGAAGAGGCAAAATGAATTTCTGACGGCAGACAAGAGGTA 1154

QY 666 ----- 665

Db 1155 AGTCCTAGAGCTGGGAAGGGCTTGGAACTAATGCCCTAGGGTCTGATTCATGTCTCTGCC 1214

QY 666 -----GAAAGTTGCCCATTTGTAATGAAGATGATGAGCTTTGTGCCATCATTTGCC 716

|||||

Db 1215 CTGACCACAGGAAGTTGCCCATTTGTAATGAAGATGATGAGCTTTGTGCCATCATTTGCC 1274

QY 717 CGGACAGACCTGAAGAAGATCGGGACTACCCACTAGCCTCCAAAGA--TGCCAAGAAAC 774

Db 1275 CGACAGACCTGAGAGAATCGGAGCTACCCACTAGCCTCCAAAGAAATGCCCAAGAAG 1334
QY 775 AGCTGCTGTGTGGGCGAGCCATTGGCAGCTCATGAGATGACAGATATAGGCTGAGCTTGC 834
Db 1335 AGCTGCTGTGTGGGCGAGCCATTGGCAGCTCATGAGATGACAGATATAGGCTGAGCTTGC 1394
QY 835 TCGCCAGGCTGTGTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCCATCTTCC 894
Db 1395 TCGCCAGGCTGTGTGATGTAGTGTGTTTGGACTCTTCCAGGGAATTCCATCTTCC 1454
QY 895 AGATCAATATGATCAAGTACATCAAGAACAATACCCTAATCTCCAAATCATTTGAGGCA 954
Db 1455 AGATCAATATGATCAAGTACATCAAGAACAATACCCTAATCTCCAAATCATTTGAGGCA 1514
QY 955 ATGTGTCACCTGCTGCCAGGCGCAAGACCTCATTTGATGACAGTGTGATGCCCTGCGGG 1014
Db 1515 ATGTGTCACCTGCTGCCAGGCGCAAGACCTCATTTGATGACAGTGTGATGCCCTGCGGG 1574
QY 1015 TGGGCAATGGGAAGTGGCTCCATCTGCATTATCCAGGAAG----- 1053
Db 1575 TGGGCAATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGATCCCTCCAG 1634
QY 1054 -----TGCTGGCCT 1062
Db 1635 ACATAAGTCCACAGAGCCCAATGCCCTTCTACTGTACAGGGTTCCTATATGTGCGCCT 1694
QY 1063 GTGGGCGGCCCCAAGCAACAGCAGTGTACAAGTGTATGATATGCAGGCGCTTTGGTG 1122
Db 1695 GTGGGCGGCCCCAAGCAACAGCAGTGTACAAGTGTACAGAGTGTACAGATATGCAGGCGCTTTGGTG 1754
QY 1123 TTCCGGTTCATTTGCTGATGAGAGAATCCAAATGTGGGTATATTGCCGAAGCCTTGGCCC 1182
Db 1755 TTCCGGTTCATTTGCTGATGAGAGAATCCAAATGTGGGTATATTGCCGAAGCCTTGGCCC 1814
QY 1183 TTGGGGCCTCCACAGTCATGATGGGCTCTCTCTGGC 1219
Db 1815 TTGGGGCCTCCACAGTCATGATGGGCTCTCTCTGGC 1851

RESULT 12
US-09-925-302-386
; Sequence 386, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 386
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (412)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (504)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (511)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (528)
; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc feature
; LOCATION: (548)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (555)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (569)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (589)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (617)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (631)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (666)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (672)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-386

Query Match 33.0%; Score 545.6; DB 10; Length 674;
Best Local Similarity 94.3%; Pred. No. 1.1e-160;
Matches 593; Conservative 0; Mismatches 33; Indels 3; Gaps 3;

QY 156 ATTCTCCCTGGGTACATGCACTTCACTGCAGACCGAGTGGAAGCTTCTGCTGACC 215
Db 2 ATTCTCCCTGGGTACATGCACTTCACTGCAGACCGAGTGGAAGCTTCTGCTGACC 61
QY 216 AAGAAATCACTCTTAAGACCCCACTGGTTTCTCTCCCATGGACACAGTCACAGAGCT 275
Db 62 AAGAAATCACTCTTAAGACCCCACTGGTTTCTCTCCCATGGACACAGTCACAGAGCT 121
QY 276 GGGATGGCCATAGCAATGGCGCTTACAGGCGGTATGGCTTCATCCACCAACTGTACA 335
Db 122 GGGATGGCCATAGCAATGGCGCTTACAGGCGGTATGGCTTCATCCACCAACTGTACA 181
QY 336 CCTGAATTCAGGCGCAATGAAGTTCGGAAGTGAAGAATATGAACAGGATTCATCACA 395
Db 182 CCTGAATTCAGGCGCAATGAAGTTCGGAAGTGAAGAATATGAACAGGATTCATCACA 241
QY 396 GACCCGTGTGCTCCTCAGCCCCCAAGGATCGCGCTGCGGATGTTTTTGAGGCCAAGCCCCG 455
Db 242 GACCCGTGTGCTCCTCAGCCCCCAAGGATCGCGCTGCGGATGTTTTTGAGGCCAAGCCCCG 301
QY 456 CATGCTTTCTGCGGTATCCCAATCACAGACACAGCCGAGTGGGAGCCGCTTGTGGGC 515
Db 302 CATGCTTTCTGCGGTATCCCAATCACAGACACAGCCGAGTGGGAGCCGCTTGTGGGC 361
QY 516 ATCATCTCCTCCAGGAGCATTTTCTCTCAAGAGAGGAACATGACTGTTCTTGGAA 575
Db 362 ATCATCTCCTCCAGGAGCATTTTCTCTCAAGAGAGGAACATGACTGTTCTTGGAA 421
QY 576 GAGATAATGACAAGAGGAGACTTTGGTGTAGCCCCCGCAGCATCACACTGAAGGAG 635
Db 422 GAGATAATGACAAGAGGAGACTTTGGTGTAGCCCCCGCAGCATCACACTGAAGGAG 481
QY 636 GCAATGAATTTCTGACGCGCAGCAAGAAGGGAAGTTGCCCATTTGTAATGAGATGAT 695
Db 482 GCAATGAATTTCTGACGCGCAGCAAGAAGGGAAGTTGCCCATTTGTAATGAGATGAT 540
QY 696 GAGCTTGTGGCATCATTTGCCCGGACAGACCTGAAGAAGATCGGAGCTACCCACTAGCC 755
Db 541 GAGCTTGTGGCATCATTTGCCCGGACAGANCTGAAGAAGATCGGG-CTANCCACTAGCT 598
QY 756 TCCAAGATGCCAAGAAGAGCTGCTGTG 784
Db 599 TCAAGATGCCAAGAAGANTGTGGGTGGG 627

RESULT 13
US-09-853-918-44
; Sequence 44, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Keystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: DB24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-853-918-44

Query Match 31.1%; Score 513.6; DB 10; Length 1155;
Best Local Similarity 76.5%; Pred. No. 1.7e-150;
Matches 630; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

QY 769 AGAAGAGCTGCTGTGTGGGACAGCATTTGGCAGCTCATGAGGATGACAAGTATAGCTGG 828
Db 332 ACAAAACCTGCTGTGTGGGACAGCTGTGGGACACCCGTGAGGATGACAATACCGTCTGG 391
QY 829 ACTTGCTCGCCAGCGCTGTGTGATGTAGTGTCTTTGACCTCTTCCAGGAAATTTCCA 888
Db 392 ACCTGCTACCCAGGCGGCGCTGACGCTCATAGTCTTGAGCTCGTCCCAAGGGAATTCGG 451
QY 889 TCTTCAGATCAATATGATCAAGTACATCAAGACAATACCCTAATCTCCAAGTCATTG 948
Db 452 TGTATCAATCGCCATGTTGATATCATCAAAACAGAGTACCCCACTCCAGGTGATTG 511
QY 949 GAGGCAATGTGTCACCTGCTGCCAGGCCAAGAACCTCATTTGATGCAAGGTGTGATGCC 1008
Db 512 GGGGAACGTGTGTACAGACAGCCCAAGCAAGACCTGATTGATGCTGTGTGACGGCG 571
QY 1009 TGGCGGTGGGCATGGGAAGTGGCTCCATCTGCATTATCCAGGAAGTGTGCGCTGTGGG 1068
Db 572 TGGCGGTGGGCATGGGCTGCGGCTCATCTGCATCACCCAGGAAGTGTGCGCTGTGTC 631
QY 1069 GGCCCAAGCAACAGCAGTGTACAAAGTGTATGAGTATGACAGGCGCTTTGTTCCGG 1128
Db 632 GGCCCAAGGCACTGCTGTACAAAGTGTGCTGAGTATGCCCGGCTTTGTTGCCCA 691
QY 1129 TCATTGCTGATGGAGAAATCGGGTCATATTGCCAAAGCCTTGGCCCTTGGGG 1188
Db 692 TCATAGCCGATGGCGGCATCCAGACCGTGGGACACGTGTCAAAGGCCCTGGCCCTGGAG 751
QY 1189 CCTCAGAGTCATGATGGGCTCTCTCTGGCTGCCACCACTGAGCGCCCTGTGTAATCT 1248
Db 752 CCTCAGAGTCATGATGGGCTCCTCTGCTGGCCGACACTACGAGGCGCCCTGGCGAGTACT 811
QY 1249 TCTTTTCGATGGGATCCGGCTAAAGAAATATCGCGTATGGGTTCTCTCGATGCCATGG 1308
Db 812 TCTTTCAGACGGGGTGCAGTCAAGAAATACCGGGCATGGGCTCACATGATGCCATGG 871
QY 1309 ACAAGCACTCAGCAGCCAGAACAGATATTTTCAGTGAAGCTGACAATAATCAAGTGGCCC 1368
Db 872 AGAAGAGCAGCAGCAGCCAGAAACGATACTTCAGCGAGGGGGATAAAGTGAAGATCGCGC 931

QY 1369 AGGAGTGTCTGTGCTGTGACAGACAAGGGTCAATTCACAAATTTGTCCCTTACTGA 1428
Db 932 AGGTGTCTCGGGCTCCATCCAGACAAGGATCCATTCAGAAAGTTGTCGCCCTACTCA 991
QY 1429 TTGCTGGCATCCAACACATCATGCCAGACATTTGTGCCAAGAGCTTGAACCAAGTCCGAG 1488
Db 992 TAGCAGGCATCCAACACAGCGCTGCCAGGATATCGGGCCGACCTGTCTGTCTTCGGT 1051
QY 1489 CCATGATGTACTCTGGGAGCTTAAGTTTGAGAAGAAAGTCCTCAGCCAGGTGAAG 1548
Db 1052 CCATGATGTACTCAGAGAGAGCTCAAGTTTGAGAAGCGGACCATGTCCGCCAGATTGAGG 1111
QY 1549 GTGGCTCCATAGCCTCCATTCGTATGAGAAGCGGCTTTCTGA 1592
Db 1112 GTGGTGTCCATGGCCTGCACCTTTACGAAAAGCGGCTGTACTGA 1155

RESULT 14
US-09-879-536-844
; Sequence 844, Application US/09879536
; Patent No. US20020144298A1
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steilmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/879,536
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/088,801
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 844
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(675)
; OTHER INFORMATION: n = A,T,C or G
US-09-879-536-844

Query Match 25.4%; Score 420.6; DB 10; Length 675;
Best Local Similarity 95.8%; Pred. No. 1.7e-121;
Matches 432; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 331 GTACACCTGAATTCCAGGCCAATGAAGTTCCGAAAGTGAGAAATATGAACAGGGATTC 390
Db 2 GTACACCTGAATTCCAGGCCAATGAAGTTCCGAAAGTGAGAAATATGAACAGGGATTC 61
QY 391 TCACAGACCCTGTGTCTCAGCCCCAAGGATCGCTGCGGATGTTTTTGAGGCCAAG 450
Db 62 TCACAGACCCTGTGTCTCAGCCCCAAGGATCGCTGCGGATGTTTTTGAGGCCAAG 121
QY 451 CCCGGCATGTTTCTGCGTATCCCAATCAGACACAGCGCGGATGGGAGCGGCTGG 510
Db 122 CCCGGCATGTTTCTGCGTATCCCAATCAGACACAGCGCGGATGGGAGCGGCTGG 181
QY 511 TGGGCATCATCTCTCCAGGGACATTTGTTTCTCAAAAGCAGAGAACATGACTGTTTCT 570
Db 182 TGGGCATCATCTCTCCAGGGACATTTGTTTCTCAAAAGCAGAGAACATGACTGTTTCT 241

QY 571 TCGAAGACATATATGACAAAGAGGAGACTTGTGTAGCCCCCGGAGCATCACACTGA 630
Db 242 TGGAGAGATATATGACAAAGAGGAGACTTGTGTAGCCCCCGGAGCATCACACTGA 301
QY 631 AGGAGCAATGAATTTCTGACGGCAGCAAGAAGGAAAGTTGCCCATTTGTAATGAAG 690
Db 302 AGGAGCAATGAATTTCTGACGGCAGCAAGAAGGAAAGTTGCCCATTTGTAATGAAG 361
QY 691 ATGATGAGCTTGTGGCCATCATTTGCCCGAGACAGACCTGAAGAAGAAATGGGACTACCAC 750
Db 362 ATGATGAGCTTGTGGCCATCATTTGCCCGAGACAGACCTGAAGAAGAAATGGGACTACCAC 421
QY 751 TAGCCTCCAAGATGCCAAGAAGACCTGCT 781
Db 422 TAGCCTTCCAAGATGCCAAGAAGACCTGCT 452

RESULT 15
US-10-076-157-7
; Sequence 7, Application US/10076157
; Publication No. US20030027309A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Suelberger, Harald
; APPLICANT: Joeffken, Hans Wolfgang
; APPLICANT: Doval, Jose Luis Revuelta
; APPLICANT: Jimenez, Alberto
; APPLICANT: Garcia, Maria Angeles Santos
; TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use the
; TITLE OF INVENTION: in
; TITLE OF INVENTION: microbial riboflavin synthesis
; FILE REFERENCE: 48684DIY
; CURRENT APPLICATION NUMBER: US/10/076,157
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 09/212,247
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: WordPerfect v. 6.1
; SEQ ID NO 7
; LENGTH: 3616
; TYPE: DNA
; ORGANISM: Ashbya gossypii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 864..1316
; NAME/KEY: CDS
; LOCATION: 1478..2592
; US-10-076-157-7

Query Match 24.8%; Score 410.2; DB 9; Length 3616;
Best Local Similarity 62.2%; Pred. No. 9.7e-118;
Matches 709; Conservative 0; Mismatches 403; Indels 27; Gaps 3;

QY 465 TGGCGTATCCCAATCAGACAGACAGCCGGATGGGAGCCGCTTGGTGGCATCATCTCC 524
Db 1460 TGTACTAACAATCAGATGATGCAAGCCGACCGGAAGCTGCAGGGCATCATCAG 1519
QY 525 TCCAGGAGCATTTGATTTTCTCAAGAGGAGGAACATGACTGTTCTTGAAGAGATAATG 584
Db 1520 TCCCGTGCATCCAGTTTGTTCAGACGAG-----ACCTGCTTGTGTCTGAG 1567
QY 585 ACAAGAGGGAAGACTTGTGTAGCCCCCGCAGCATCACACTGAAGAGGCAATGAA 644
Db 1568 ATCATGACCAAGAGCGTCACTGGAAGCAGGCGATCAACCTCGAGAGGGAACACAG 1627
QY 645 ATTCTGACGCGCAGCAGAGGAAAGTTGCCCATTTGTAATGAAGATATGAGCTTGTG 704
Db 1628 ATCTGAAGAACACCAAGAGGGAAGCTGCCAATTTGTGACGAGGCGGCTGCCTGTG 1687
QY 705 GCCATCATTTGCCGAGCAGAGACCTGAAGAAGATCGGACTACCACTAACCCTCCAAGAT 764
Db 1688 TCCATGCTTTCGAGAACTGACTTGATGAAGAACACAGTCTACCCATTTGCCCTCCAAGTCT 1747

QY 765 GCCAA---GAACAGCTGCTGTGGGGCAGCCATTGGCAGCTATGAGGATGACAAGTAT 821
Db 1748 GCCGACACCAAGCAGCTGCTGTGGTGTCTGCGATCGGACATCGACGCGGACAGGAG 1807
QY 822 AGGCTGACTTGCCTCGCCAGCCTGCTGTGATGTAGTGTGTTTGACTCTTCCAGCA 881
Db 1808 AGACTGGGAGCTGTGTCGAGGCGGCTTGACGTTGTTGCTAGACTCTCGCAGGCT 1867
QY 882 AATTCCATCTTCCAGATCAATATGATCAAGTACATCAAGAGCAAAATACCTAATCTCAA 941
Db 1868 AACTCGGCTTCCAGATCAACATGATCAAGTGAATCAAGAGAGACCTTCCAGACCTGAG 1927
QY 942 GTCATTTGAGGCAATGTGTGCTGCTGCTGCCAGGCAAGAACCTCATTTGATGAGGTGTG 1001
Db 1928 GTCATTTGAGGCAACGTGTGCTGCTGCTGCCAGGCTGCTGATGATCCAGCGCGGCA 1987
QY 1002 GATGCCCTGCGGGTGGGATGGGAAGTGGCTCCATCTGCATTTCCAGGAAGTGTGGCC 1061
Db 1988 GACGGGTGCTGATCGGTATGGGCTGCTGCTCATCTGATGATCAGGAGTGTGGCC 2047
QY 1062 TGTGGGCGCCCAAGCAACAGCAGTGTACAAGGTATGATGATGACAGGCGCTTTGGT 1121
Db 2048 TGTGTAGACCAAGAGGTATCCGCTGTCTACAACGTACCGCATTTGCCAACCAGTTTGGT 2107
QY 1122 GTTCCGCTCATTTGCTGATGAGGAATCCAAATGTGGTCAATTTGCCAAAGCCTTGCC 1181
Db 2108 GTGCCATGATTTGCTGACGGTGTGTCAGAAACATCGGGCAGACTTACCAAAAGCTATGCT 2167
QY 1182 CTTGGGCTTCCACAGTCAATGATGGGCTCTCTCTGCTGCTGCCACCACTGAGGCCCTGT 1241
Db 2168 CTTGGGCTTCCACAGTCAATGATGGGCTCTCTCTGCTGCTGCCACCACTGAGGCCCTGT 2227
QY 1242 GAATACTTCTTTTCCGATGGATCCGGCTAAAGAAATATCGGGTATGGGTTCTCTGAT 1301
Db 2228 GAGTACTTCTTCCAGGAGCGGGAAGAGACTGAAGACCTACAGAGTATGGGCTCCATGAC 2287
QY 1302 GCCATGACAAGCAGCTCAGACAGCCAGAA-----CAGATATTTCAAGTGAAGCT 1349
Db 2288 GCCATGACAAGCAGCTGATGTAAGGTAACGCCGCTACCTCCGTTACTTCTGAGTCT 2347
QY 1350 GACAAATCAAAAGTGGCCCGCAGGAGTCTGTGCTGTGACAGACAAAGGTCATTCAC 1409
Db 2348 GACAAGTCTCTGTCGCTCAGGGTCTTACTGTTCTGTGATGACAAAGGCTCCATCAAG 2407
QY 1410 AATTTGTCCCTTACCTGATTTGCTGCAATCCACACTCATGCCAGACATTTGTGCCAAG 1469
Db 2408 AAGTACATTTCCATATCTGTACAAATGGTCTACAGCACTCGTCCAGATATCGGTGTGCC 2467
QY 1470 AGCTTGACCCAAGTCCGAGCCATGATGTAATCTGTGGGAGCTTAACTTTGAGAAGAGAACG 1529
Db 2468 TCTCTAGTGAAGTTCAAGAGAGAGGCTGACTCTGGCTCGGTACAGATTGAGTTCAAGACT 2527
QY 1530 TCCTCAGCCCAAGGTGAAGGTGGCTGCCATTAAGCTTCCATTTGATGAAGAGCGGCTTTT 1588
Db 2528 CCATCTGCCCAAGTTGAGAGGTGTGTGCACAACTTGCACTTCTTACGAGAAGCGGCTATT 2586

Search completed: February 12, 2003, 23:36:51
Job time : 159 secs

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